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GenCore version 4.5
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OM protein - protein search, using sw model

7, 2002, 12:31:45; Search time 14.38 Seconds (without alignments) 783.994 Million cell updates/sec Run on:

US-09-016-869B-35 760 1 MEPSADWLATAAARGRVEEV......TRGSNHARIDAAEGPSDIPD 148 Title: Perfect score: Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database :

pirl:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	cyclin dependent k		CDK4 inhibitor p14	p16INK4a - mouse	cyclin-dependent k	CDK4/CDK6 inhibito	cyclin-dependent k	CDK4/CDK6 inhibito	CDK6 inhibitor p18	gene p15INK4B prot		ankyrin, erythrocy	ankyrin - mouse	ankyrin 1, erythro	1,		o um		UIII C	'n		'n		ankyrin 3, long sp	-related	elegans ankyrin-re	ankyrin-related un	•	probable ankyrin [
ΙD	JE0141	178845	B55479	158352	A57378	A57379	B57378	B57379	A55479	152720	S37431	S37771	149502	B35049	A35049	SJHUK	Θ	137275	(4	T42714		T42713	T42716	A55575	A57282	S	534	534	D84448
DB	2	7	~	7	7	7	7	~	7	7	7	7	7	7	7		7	Н	7	7	7	~	7	7	7	7	~	7	7
Length	156	130	138	167	164	166	166	168	168	41	3924	1848	1862	1856	1880	1881	857	1423	838	1765	1940	1943	1961	4377	1786	1815	1867	2039	247
% Query Match	99.1	9.69	68.7								•														16.8		16.8	٠	•
Score	753	529	522	461.5	258	249	244	231.5	228.5	209	158	137.5	137.5	133.5	133.5	133.5	131	130.5	130	130	130	130	130	128	127.5		127.5		126
Result No.	1	7	e	4	Ŋ	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24			27		29

A; Gene: GDB:CDKN2A; CDK4I; MLM; P16; INK4; MTS1; CMM2; CDKN2
A; Cross-references: GDB:335362; OMIM:600160
A; Map position: 9p21-9p21
C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat howology; EGF homol C; Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

notch4 - mouse	hypothetical prote	related to 26s pro	probable potassium	hypothetical prote	GA-binding protein	GA-binding protein	nuclear respirator	nuclear respirator	nuclear respirator	nuclear respirator	hypothetical prote	ankyrin - fruit fl	ankyrin-like prote	potassium channel	transmembrane prot
T09059	T15888	T50984	D84650	T23213	C40858	B40858	C48146	I38744	138743	138741	T32930	T13940	D82654	T52046	842612
7	~	7	ď	7	~	7	7	7	7	7	7	~	C	~	7
1964	209	237	888	476	347	382	347	348	360	395	1435	1549	1058	828	2437
16.4	16.4	15.9	15.9	15.8	15.6	15.6	15.5	15.5	15.5	15.5	15.4	15.3	15.2	15.0	15.0
125	124.5	121	121	120	118.5	118.5	117.5	117.5	117.5	117.5	117	116	115.5	1.14	114
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1 JE0141 cyclin dependent kinase inhibitor - human
	N;Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor
	C.Decersor, monto suprator (mar.) (mar.) (mar.) (c.) Accession: JE0141; 159268; 539359; 159585; JC5679
	R; Huang, C.G.; Deng, W.; Fu, J.L. Chin. J. Biotechnol. 13, 105-107, 1997
	A, Title: Molecular cloning and sequencing of P16 ink4 cDNA from hela cell.
	A. Accession: JE0141
	A; Molecule type: mRNA A: Residues: 1-156 < HUA>
	A/Experimental source: Hella cell
	R: (Namodo, A.; Demetrick, D.J.; Spillare, E.A.; Hajwara, K.; Hussain, S.P.; Bennett,
	A.Title: Mutations and altered expression of pi61NK4 in human cancer.
	A; Reference number: 159268; MUID:95062202
	A. CESTICE LOSTON DOLL CHORUM - Francisted from CD/FMDI /DNDI
	A. Molecule tyre. DNA A. Molecule tyre.
	A; Residues: 1-152 < OKA>
	A; Cross-references: GB:L27211; NID:9558656; PIDN:AAA92554.1; PID:9558657
	A;Note: the sequence is revised in GenBank entry HUMINK4X, release 113.0, PIDN:AAA925
	R;Serrano, M.; Hannon, G.J.; Beach, D.
	A:Title: A new requiatory motif in cell-cycle control causing specific inhibition of
	A; Reference number: S39359; MUID:94081956
	A; Accession: S39359
	A, Status: preliminary
	A MOLECULE TYPE: INFA CETE A DOSISTING 0-24 'V' 26-166 CETE
	A:Note: this sequence is corrected in reference 159268
	R; Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.;
	Science 264, 436-440, 1994
	A 7/Title: A cell cycle regulator potentially involved in genesis of many tumor types.
	A:Accession: 159585
	A; Status: translation not shown; translated from GB/EMBL/DDBJ
	A; Molecule type: DNA
	A; Residues: 51-152 < KAM>
	C)Commence: This process sometimes the activity of cyclin bi/cbk4 and cyclin bi/cbk6 ki
_	A.Generation GDB:CDKN2A: CDK41: MLM: P16: INK4: MTS1: CMM2: CDKN2

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homod

EGF

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Gaps

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A; Accession: 18183
A; Status: translation not shown; translated from GB/EMBL/DDBJ
A; Status: translation not shown; translated from GB/EMBL/DDBJ
A; Status: translation not shown; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; True: Fes. 54, 6353-638, 1994
A; True: Deletion of pl6 and pl5 genes in brain tumors.
A; Reference number: 152713; MUID:95079408
A; True: Deletion of pl6 and pl5 genes in brain tumors.
A; Reference number: 152713; MUID:95079408
A; Tatus: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-52 < RES>
A; Corossion: 1522 RES>
A; Residues: 1-52 < RES>
A; Residues: 1-52 < RES>
A; Genetics:
A; Genetic
                                                                                                           Q.; Harshman, K.; Tavtigian, S.V.;
A;Cross-references: GB:L36844; NID:9556197; PIDN:AAA50282.1; PID:9556198
A;Experimental source: HaCar cells
R;Kamb, A.; Grnis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V. Science 264, 436-440, 1994
A;Title: A cell cycle regulator potentially involved in genesis of many tumor types.
A;Reference number: 159585; MUID:94204645
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C;Species: Mus Sp. (mouse)
C;Species: Mus Sp. (mouse)
C;Species: Mus Sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C;Accession: 158352
R;Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, Oncogene 11, 635-645, 1995
A;Title: Cloning and characterization of murine p16INK4a and p15INK4b genes.
A;Reference number: 158352; MUID:95380169
A;Accession: 158352
A;Accession: I58352
A;Access
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C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A) Map position: 9p21-9p21
C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
C; Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 CADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAGYLR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 522; DB 2; Length 13
Pred. No. 1.2e-42;
4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross_references: GB:S79251; NID:g1087090; PID:g1087091
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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Best Local Similarity 63.2%; Pred. No. 8.5e-37;
Matches 98; Conservative 16; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.7%;
llarity 85.5%;
Conservative
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Matches 106; Conserv
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N;Alternate names: CDK6-associated protein pl5(INK4B); cyclin-dependent kinase inhibitor
C;Species: Homo saplens (man)
C;Species: Janar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Ju1-2000
C;Accession: B55479; MJD:95095079
A;Recession: B55479
A;Recession: B55479
A;Residues: 1-138 <GMA>
A;Residues: 1-138 <GMA>
A;Reference number: Botential effector of TGF-beta-induced cell cycle arrest.
A;Recession: S47593; MJD:94359613
A;Recession: S47593
A;Residues: 1,-19, TP', 22, 24-31, 'HSW', 35-138 <HAN>
A;Residues: 1,-19, TP', 22, 24-31, 'HSW', 35-138 <HAN>
A;Residues: 1,-19, TP', 24, 24, 31, 'HSW', 35-138 <HAN>
A;Residues: 1,-19, TP', 22, 24-31, 'HSW', 35-138 <HAN>
A;Residues: 1,-19, TP', 22, 24-31, 'HSW', 35-138 <HAN>
A;Residues: 1,-10, TP', 22, 24-31, 'HSW', 35-138 
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C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
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                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                       Gaps
                                                                                                                                                                                                                       1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
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                                              Length 156;
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                                                                                                                                       Indels
                                              Score 753; DB 2; I
Pred. No. 1.5e-64;
0; Mismatches 1;
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Pred. No. 2.5e-43;
4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.6%;
ilarity 88.3%;
Conservative 4
                                                        99.1%;
99.3%;
                                                        Query Match 99.1
Best Local Similarity 99.3
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Matches 106;
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```

К.Н.

EGF homol

ä;

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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 20-Sep-1999
C;Accession: B57379
Mol. Cell. Biol. 15, 2672-2681, 1995
A;Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-de A;Reference number: A57379; MuID:95257948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-168 ~HIR>
A;Cross-references: GB:U19596; NID:q790566; PIDN:AAC52193.1; PID:q790567
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
C;Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                     CDK6 inhibitor with
                                                                                                                                                                                                                                                                Cyclin-dependent kinase inhibitor p19 - mouse Cyclin-dependent kinase inhibitor p19 - mouse Cypecies: Wus musculus (house mouse) Cipecies: Wus musculus (house mouse) Cipecies: Wus musculus (house mouse) Cipecesion: B57378 Richan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A. Mol. Cell. Biol. 15, 2682-2688, 1995 a novel CDK4 and CDK6 inhibi: A; Reference number: A57378; MUID:95257949 A; Reference number: A57378; MUID:95257949 A; Reference number: A57378 A; Reference number: A77378; MUID:95257949 A; Reference number: A77378; MUID:972257949 A; Reference number: A77378; MUID:97227949 A; Reference number: A77378; MUID:9791204; DIDN:AAA85437.1; PID:9791205 C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 ADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL-- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 QD-ASGTSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFLAP 128
                            PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARY 121
     65 ADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL-- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 DWLATAAARGRVEEVRALL-EAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNC 64
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                                                                                                                             129 ESDLHHRDASGLTPLELARQRGAQNL-MDILQGHMMIP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 ESDLHHRDASGLTPLELARQRGAQNL-MDILQGHMMIP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.1%; Score 244; DB 2;
43.7%; Pred. No. 4e-16;
live 18; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----RAAAGGT-----RGSNHARIDAAEGPSDIP 147
                                                                                                   -----RAAAGGT-----RGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - :== :=::
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Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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CDK4/CDK6 inhibitor p19 - mouse
CJSpecies: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A57379
C;Accession: A57379
K;Hiral, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr, C.J.
Mol. Cell. Biol. 15, 2672-2681, 1995
A;Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-depen A;Reference number: A57379; MUID:95257948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology
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                                                                                                                                                                                                              RESULT 5
A57378
Cyclin-dependent kinase inhibitor p19 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Detei 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 22-Jun-1999
C;Accession: A57378
R;Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.
Mol. cell. Biol. 15, 2682-2688, 1995
A7:Itle: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with backerence number: A57378; MUID:95257949
A;Status: preliminary
A;Molecule type: mRNA
A:Molecule type: mRNA
A:Molecule type: mRNA
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C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF
C;Keywords: cell cycle control
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EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                          61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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44.3%; Pred. No. 1.3e-16;
Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 258; DB 2;
Pred. No. 1.8e-17;
                                                                                              121 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 147
                                                                                                                             120 YLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 19p13
C; Superfamily: unassigned ankyrin
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1 Similarity 44.1%;
67; Conservative 1
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A;Cross-references: GB:U20498
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Best Local Similarity
Matches 67; Conserv
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A; Molecule type: mRNA
A; Residues: 1-166 <HIR>
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nes 70; Conserv
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1 MMMGSAQVAELLLLHGAEPNCADPATLTRPVHDAAREGFLD 41

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63 PNLKD-GTGFAVIHDAARAGFLDTVQALLEFQADVNIEDNEGNLPLHLAAKEGHLPVVEF 121

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A.Molecule type: DNA
A.Residues: 463-474, PE', 477-495 <TSE>
A.Residues: 463-474, PE', 477-495 <TSE>
A.Crossreferences: GB:M37123; DNI, 127-495 <TSE>
A.Crossreferences: GB:M37123; DSI, 127-495 <TSE>
B.Chan, W.; Kordeli, E.; Bennett, V.
J. Cell Biol. 123, 1463-1473, 1993
A.Title: 440-Kb ankyrinB: structure of the major developmentally regulated domain and A.Reference number: A49462; MUID:94075409
A.Recession: A49462
A.Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S374A.
A; Status: preliminary
A; Molecule type: mRNA
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                                                                                         ankyrin 2, neuronal long splice form - human N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythro N;Contains: ankyrin 2, short form C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #sequence_revision C;Accession: S37431; A39643; B39643; A40334; A40462; S14533; S14569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1443,358-3924 <OTT>
A;Residues: 1-1443,358-3924 <OTT>
A;Cross-references: EMBL:X56958
B;Trse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Wa Genomics 10, 858-866, 1991
A;Title: Isolabation and chromosomal localization of a novel nonerythroid ankyrin gene.
A;Reference number: A40334; MUID:92009921
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A;Map position: 4q25-4q27
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing
F;2-3424/Product: ankyrin 2, long form #status predicted <MAT>
F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MAZ>
                                                                                                                                                                                                                                                                                                                        R;Chan, W. submitted to the EMBL Data Library, September 1993 A;Reference number: 837431
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F;96-128/Domain: ankyrin repeat homology <ANU2>
F;129-161/Domain: ankyrin repeat homology <ANU3-
F;129-161/Domain: ankyrin repeat homology <ANU3:
F;162-190/Domain: ankyrin repeat homology <ANU04:
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F;529-561/Domain: ankyrin repeat
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F;364-396/Domain: ankyrin repeat
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A; Residues: 1-2077 <0T1>
A; Cross-references: GB:X56957
A; Accession: B39643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;397-429/Domain: ankyrin
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A; Residues: 1-3924 <RES>
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C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-May-2000
C; Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-May-2000
C; Accession: I52720
R; Knapek, D. F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.
Cancer Res. 55, 1607-1612, 1995
A; Title: Association of rat p151NK4B/p161NK4 deletions with monosomy 5 in kidney epithel A; Reference number: I52720; MUID:95228036
A; Accession: I52720
A; Ascession: I52720
A; Association: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residuas: 1-41 CRES.
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                                                                                                                                                                                                                                                             CDK6 inhibitor p18 - human N.Alternate names: cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent kinase C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 23.Mar-1995 #sequence_revision 23.Mar-1995 #text_change 20.Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                             R;Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G. Genes Dev. 8, 2939-2952, 1994
A;Title: Growth suppression by p18, a p16(INK4/WIS1)- and p14(INK4B/WIS2)-related CDK6
A;Reference number: A55479; MUID:95095079
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A;Cross-references: GDB:594931
A;Map position: 1932-1932
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
C;Superfamily: unassigned control; protein kinase inhibitor; tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARY 121
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 228.5; DB 2;
; Pred. No. 1.2e-14;
22; Mismatches 60;
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Best Local Similarity 97.6%;
Matches 40; Conservative
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122 LVKHTASNVGHRNHKGDTA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match .30.1%;
Best Local Similarity 40.3%;
Matches 56; Conservative 2;
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122 LRAAAGGTRGSNHARIDAA 140
                                                  122 LMKHTACNVGHRNHKGDTA 140
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A; Residues: 1-168 <GUA>
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R.White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
Mamm. Genome 3, 281-285, 1992.
A,Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory
A,Reference number: 149502; MUID:92345717
A;Reference number: 149502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 149502
                                                                                                                                                                         67 PATLTRPVHDAAREGFLDTL-VVLHRAGARLDVRDAW-GRLPVDLAEELGHRDVARYL-- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: M84756; NID: 9191939; PIDN: AAA37236.1; PID: 9191940
          8 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQV-MMMGSARVAELLLLHGAEPNCAD
                                                Length 1862;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. Superfamily: ankyrin; ankyrin repeat homology C; Keywords: alternative splicing C; Keywords: Annology C; Keywords: alternative splicing C; 
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<AN18>
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                                                                                                                                                                                                                                                               123 ---RAAAGGTRGSNHARIDAAEGPSDI 146
                                                                                                                                                                                                                                                                                                     | | : | | : | | : | 628 YGGSANAESVQGVTPLHLAAQEGHTEM 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homology
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34.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.1%
Best Local Similarity 34.7%
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-1862 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;498-530/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ankyrin - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics
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G:Species: Mas masculus (house mouse)

G:Decies: Was masculus (house mouse)

C:Decies: Was masculus (house mouse)

C:Accession: 53771

R:Birkenmeler: C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.

J. Blol. Chem. 266, 9533-9540, 1993

A.Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found and A.Reference number: 33771; MUID:93252825

A.Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found and A.Reference number: 33771; MUID:93252825

A.Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found and A.Residues: 1'1840 *CBR*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 PATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL--RA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQV-MMMGSARVAELLLLHGAEPNCAD 66
                                                                                                                                                                                                                                                                                                                                                                                                      4;
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                                                                                                                                                                                                                                                                                                                                                                                               59; Indels
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                                                                                                                                                                                                                                                                                                                              Score 158; DB 2;
Fred. No. 2.1e-06;
18; Mismatches 59
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; Pred. No. 8e-05;
17; Mismatches (
      <AN16>
<AN17>
<AN18>
                                                                                                    <an19><an20><an21><an21></a>
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F;562-594/Domain: ankyrin repeat homology F;595-621/Domain: ankyrin repeat homology F;628-660/Domain: ankyrin repeat homology F;661-693/Domain: ankyrin repeat homology F;727-754/Domain: ankyrin repeat homology F;767-792/Domain: ankyrin repeat homology F;760-792/Domain: ankyrin repeat homology F;760-792/Domain: ankyrin repeat homology
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Best Local Similarity 34.7%;
Matches 51; Conservative 17
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ankyrin repeat
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Best Local Similarity
Matches 48; Conserv
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587 AAADSAGKN 595
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F;737-769/Domain:
F;770-802/Domain:
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E;733-765/Domain: ankyrin repeat
E;766-798/Domain: ankyrin repeat
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                                                                                                            A; Status: preliminary
A; Molecule type: mRNA
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Job time:
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A;Title: cDNA sequence for human erythrocyte ankyrin.
A;Reference number: A35049; MUID:90175370
A;Reference number: B35049
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1856 < LAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GDB:LNB77; OMIM:182900
A,Map position: 8p11.2-8p11.2
C;Superfemily: ankyrin; ankyrin repeat homology
C;Superfemily: ankyrin; ankyrin repeat homology
C;Superfemily: ankyrin repeat homology carlos
F;2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted cMA2>
F;2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted cMA2>
F;2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted cMA2>
F;10-142/Domain: ankyrin repeat homology cAN03>
F;110-142/Domain: ankyrin repeat homology cAN03>
F;110-142/Domain: ankyrin repeat homology cAN05>
F;205-237/Domain: ankyrin repeat homology cAN05>
F;207-204/Domain: ankyrin repeat homology cAN05>
F;218-270/Domain: ankyrin repeat homology cAN10>
F;310-356/Domain: ankyrin repeat homology cAN10>
F;310-356/Domain: ankyrin repeat homology cAN11>
F;403-435/Domain: ankyrin repeat homology cAN13>
F;405-534/Domain: ankyrin repeat homology cAN15>
F;505-534/Domain: ankyrin repeat homology cAN16>
F;505-534/Domain: ankyrin repeat homology cAN16>
F;505-501/Domain: ankyrin repeat homology cAN16>
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                   N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
N;Contains: ankyrin 2.2, erythrocyte
C;Species: Homo sapiens (man)
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATLTRPVHDAAREGFLDTL-VVLHRAGARLDVRDAW-GRLPVDLAEELGHRDVARYL-- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69; Indels 11;
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35.4%; Pred. No. 0.00019;
Live 15; Mismatches 69;
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<AN22>
<AN23>
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splice form 3 - human
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homology
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Best Local Similarity
Matches 52; Conserv
   erythrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: ANK1; ANK
                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
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      ankyrin 1,
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Rilambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C. Rilambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; 1990
A;Title: cDNA sequence for human erythrocyte ankyrin.
A;Reference number: A35049; MUID:90175370
A;Accession: A35049
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1880 <LAM>
A; Cross -references: GB:M2880
C; Genetics:
C; Genetics:
A; Gene (CB: MR)
A; Cross -references: GB:L18737; OMIM:182900
A; Gene (CB: MR)
A; Cross -references: GDB:L18737; OMIM:182900
A; Map position: Bplil.2 Bplil.2
C; Superfamily: ankyrin; ankyrin repeat homology
C; Keywords: alternative splil.2 Bplil.2
C; Superfamily: ankyrin repeat homology <AN01>
F; 2-1580/Product: ankyrin repeat homology <AN02>
F; A4-76 Domain: ankyrin repeat homology <AN02>
F; A10-142/Domain: ankyrin repeat homology <AN03>
F; A10-142/Domain: ankyrin repeat homology <AN05>
F; A10-142/Domain: ankyrin repeat homology <AN05>
F; A10-427/Domain: ankyrin repeat homology <AN08>
F; A10-427/Domain: ankyrin repeat homology <AN08>
F; A10-427/Domain: ankyrin repeat homology <AN09>
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GenCore version 4.5

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OM protein - protein search, using sw model

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Title:

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Sequence:

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Listing first 45 summaries

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Sopfir N., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
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MEDLINE-97472457; Pubmed-9328469;
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[49]
ABTANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                               Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L., Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.; "Novel germline plfnnkd allele (Aspl45Cys) in a family with multiple pancreatic carcinomas:";
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A -> P (IN A LUNG TUMOR AND MELANOMA).
/FTIG=VAR_001410.
A -> S (IN A BILLARY TRACT TUMOR).
                                                                                                                                                                                                                                                             Gretarsdottir S., Olafsdottir G.H., Borg A.;

"Filve novel somatic CDRN2/P16 mutations identified in melanoma,
"Filve novel somatic CDRN2/P16 mutations identified in melanoma,
"Filve novel the pancreas.";

Hum. Mutat. 12:212-212(1998)

-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS
ABILITY TO INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS
ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.
-!- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.
-!- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.
-!- DISEASE: CDKNAA MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A
WIDE RANGE OF TISSUES.
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PROSTIE; PS00081; ANK_REPEAT; FALSE_NEG.
PROSTIE; PS50297; ANK_REP_REGION; 1.
Cell cycle; Anti-oncogene; Repeat; ANK_repeat; Disease mutation;
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                   Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,
Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets
Hum. Mol. Genet. 7:941-941(1998).
                Demenais F., Bombled J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
-:- TISSUE SPECIFFCITY: EXPRESSED UBIQUITOUSLY.
-:- INDUCTION: BY TGF-BETA.
-:- SIMILARITY: BELONGS TO THE CDKNZ FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-95380169; PubMed=7651726;
Quelle D.E., Ashmun R.A., Rannon G.J., Rehberger P.A., Trono D.,
Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
"Cloning and characterization of murine p16INK4a and p15INK4b genes.";
Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncogene 14:1361-1370(1997).
-1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
                                                                                                                                                  61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                      9 MEPSADWLATAAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVWMGSARVAELLLLHGA 68
                                      Gaps
                                                                        1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGA 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAINE-G78L/G7 X DBA;
MEDLINE-G732242; Pubmed-9178896;
Malumbres M., de Castro I., Santos J., Melendez B., Mangues R.,
Serrano M., Pellicer A., Fernandez-Piqueras J.,
"Inactivation of the cyclin-dependent kinase inhibitor pl5INK4b
deletion and de novo methylation with independence of pl6INK4a
                                      ..
                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 40, Last annotation update)
CYCLIN-DEDENDEWN KINASE 4 INHIBITOR B (P14-INK4B).
  Length 156;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alterations in murine primary T-cell lymphomas.";
Score 753; DB 1;
Pred. No. 3.8e-66;
                                                                                                                                                                                                                                                                                                                                                          130 AA.
                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                            121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U66085; AAB39833.1; -.
EMBL; U66084; AAB39833.1; JOINED.
MGD; MGT:104737; CGKn2b.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 3.
SMART; SM00248; ANK; 1.
PROSITE; PS50088; ANK_IREPEAT; 1.
                                                                                                                                                                                                                                                                                                                                                            PRT;
99.1%;
99.3%;
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                  Similarity
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                      Best Local Sim
Matches 147;
                                                                                                                                                                                                                                                                                                                                                            CDN5_MOUSE
    Query Match
                                                                                                                                                                                                                                                                                                                                      CDN5_MOUSE
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--- SUBONT: HETERODIMER OF P14 WITH CDK4.
--- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
INITAATION CODONS IN THE SAME READING FRAME.
--- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN
FESTIS, BARELY BETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL
KIDNEY, ADULT KIDNEY, BRAIN, HEARF, OR SPLEEN.
--- SIMILARITY: BELONGS TO THE CDKNZ FAMILY OF CYCLIN-DEPENDENT KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       naticus norvegitus, mar.;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                            10 LATAAARGOVETVROLLEAGADPNALNRFGRRPIQVMAMGSAQVAELLLHGAEPNCADP 69
                                                                                                                                                                                                                                                                                                                                        Gaps
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SEQUENCE OF 46-86 FROM N.A.

SEQUENCE OF 46-86 FROM N.A.

MEDILINE-95228036; Pubmed-7712460;

Knapek D.F., Serrano M. Beach D., Trono D., Walker C.L.;

Rasociation of rat p151NK4B/p161NK4 deletions with monosomy 5 in kidney epithelial cell lines but not primary renal tumors.";

Cancer Res. 55:1607-1612(1995).

The following the field of t
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Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y.,
Tsuchiya H., Kikuchi Y., Mitani H.;
"Molecular genetic basis of renal carcinogenesis in the Eker rat
model of tuberous sclerosis (Tsc2).";
Mol. Carcinog. 14:23-27(1995).
                                                                                                                                                                                                                                                                                                                                        ö
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
                                                                                                                                                                                                                                                                                  Length 130;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                               7AAD60FF552BCFF9 CRC64;
                                                                                                                                                                                                                                                                            Score 529; DB 1; Le
Pred. No. 1.5e-44;
4; Mismatches 10;
PROSITE; PS50297; ANK_REP_REGION; 1.
Cell cycle; Antl-oncogene; Repeat; ANK repeat.
REPEAT 5 34
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EMBL; S77734; -; NOT_ANNOTATED_CDS.
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                                                                                ANK 1.
ANK 2.
ANK 3.
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Μ
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Best Local Similarity 88.3%;
Matches 106; Conservative
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Rattus norvegicus (Rat)
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66
100
130
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38
71 1
104 1
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                  SEQUENCE
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Best Local S
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CDN2_MOUSE
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                                                                                              Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation. CHAIN 1 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B, LONG ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-9505079; PubMed-8001816;
MEDLINE-9505079; PubMed-8001816;
MEDLINE-9505079; MICHOLIS M.A., WU X., O'Keefe C.L.,
Matera G.A., Xiong Y.;
Matera G.A., Xiong Y.;
Growth suppression by Pl8, a pl6INK4/MTS1- and pl4INK4B/MTS2-related
CDK6 inhibitor, correlates with wild-type pRb function.";
Genes Dev. 8:2939-2952(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLIHGAEPNCADP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LATAAARGQVETVRQLLEAGADPNAVNRFGRRPIQVMAMGSAQVAELLLHGAEPNCADP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAKTANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50.
MEDLINE-95188190; PubMed-7882351;
Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,
                                                                                                                                                           CYCLIN-DEPENDENT KINASE 4 INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hannon G.J., Beach D.; "pl5INK4B is a potential effector of TGF-beta-induced cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A cell cycle regulator potentially involved in genesis of many types.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KIRASE 4 INHIBITOR B (F14-INK4B) (F15-INK4B)
(MULTIPLE TUMOR SUPPRESSOR 2) (MTS2).
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MEDLINE-94204645; PubMed-8153634;
Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
Tavrigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
                                                                                                                                                                                                                                                                                                                                                            Score 524; DB 1; Length 130;
Pred. No. 4.5e-44;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                     AC45B21FA69FAD92 CRC64;
                                                                                                                                                                              SHORT ISOFORM.
FOR SHORT ISOFORM
                                                          PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94359613; PubMed-8078588;
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                                                                                                                                                                                                                                                                                                       13748 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 371:257-261(1994)
                                                                                                                                                                                                                                                                                                                                                                                                     Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
  IPR002110; ANK
  InterPro, IPR002110; ANI
Pfam; PF00023; ank; 3.
SMART; SM00248; ANK; 1.
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130 AA;
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                                                                                                                                                             46
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P42772;
                                                                                                                                                                                                  INIT_MET
REPEAT
                                                                                                                                                                                                                                                                                  REPEAT
SEQUENCE
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Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M., Xiong Y., Beach D.H., Yokota J., Harris C.C.;
"Mutations in the pichNR4/PTSI/CDKNZ, p15INK4B/MTS2, and p18 genes in primary and metastatic lung cancer.";
Cancer Res. 55:1448-1451(1995).
-:- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR. POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST.
-:- SUBUNITAL EFFECTOR NOF TGF-BETA INDUCED IN TUMOR FORMATION.
-:- DISEASE: CDKNZB MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
-:- SIMILARITY: BELONGS TO THE CDKNZ FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4).
CDKN2A OR P16INK4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 CADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAGYLR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 CADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 SDEGLASAAARGLVEKVRQLLEAGADPNGVNRFGRRAIQVMMMGSARVAELLLLHGAEBN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 522; DB 1; Length 138;
Pred. No. 7.6e-44;
4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 AA.
                                                                                                                                                                                                                                                                    INHIBITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U17075; AAC50075.1; -...
EMBL; L36844; AAA50282.1; -...
EMBL; S69805; AAD14049.1; -...
MIM; 600431; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.7%;
85.5%;
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REPEAT
REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
   MEDIINE-95380169; PubMed=7651726; Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D., Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.; Cloning and characterization of murine pl6INK4a and pl5INK4b genes."; Oncogene 11:635-645(1995).
                                                                                                                                      -!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-!- SIMILARITY: BELONGS TO THE CDKNZ FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                              SMART; SHOUSE, ANK_REPEAT; FALSE_NEG.
PROSITE; PS50297; ANK_REPE_REGION; 1.
Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CHAIN 1 167
                                                               FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE PHOSPHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6. SUBUNIT: HETEROLIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES CONTAINED CDK6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 38, Last sequence update)
. 40, Last annotation update)
KINASE 4 INHIBITOR A (CDK41) (P16-INK4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                LONG ISOFORM.
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monodelphis domestica (Short-tailed grey opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 461.5; DB 1; Length 167; Pred. No. 6.8e-38;
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88C4588A105ECB8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SHORT ISOFORM.
FOR SHORT ISOFORM
ANK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Mismatches
                                                                                                                                                                            INHIBITORS.
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(Rel. 38, Last sequ
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17870 MW;
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                                                                                                                                                                                                                                                                                                           EMBL; L76150; AAA85453.1; -.
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                                                                                                                                                                                                                                                                                                                      MGD; MGI:104738; Cdkn2a.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 3.
SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                              167
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167 AA;
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35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Best Local $
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CDN2_MONDO
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                                                                                                             Sherburn T.E., Gale J.M., Ley R.D.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
-#BILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).
-!- SUBUNIT: HFTERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
-!- INITIATION CODONS IN THE SAME READING FRAME.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation. CHAIN 1 171 CYCLIN-DEPENDENT *KINASE 4 INHIBITOR A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 SCEKLTEAAARGRTEVVTELLELGINPNAVNRFGRSAIQVMMGNVRLAAILLQYGAEPN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 TPDPTTLTLPVHDAAREGFLDTLMLLHRAGARLDVRDSWGRLPVDLAEEQGHHLVVAYLR 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYCLIN-DEPENDENT KINASE 4 INHIBITOR A, SHORT ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLHGAEPN
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Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
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Okuda T., Hirai H., Valentine V.A., Shurtleff S.A., Kidd V.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   694264F5D0F4F6CC CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
20-A0C-2001 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 408; DB 1; L
Pred. No. 1.1e-32;
9; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHORT ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 AA.
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                                                                                                                                                                                                                                                                                                                                                                                           INHIBITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002110; ANK.
Priam; PF00023; ank; 3.
PROSITE; PS50088; ANK, REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
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45
78
111
171 AA;
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Matches 83; Conserv
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                NCBI_TaxID=13616;
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P55273; Q13102;
01-OCT-1996 (Rel
01-OCT-1996 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure of human cyclin-dependent kinase inhibitor p19(INK4d): comparison to known ankyrin-repeat-containing structures and implications for the dysfunction of tumor suppressor p16(INK4a)."; structure 6:1279-1290(1998).
-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHF (1.8 ANGSTROMS).
MEDLINE-98455510; PubMed-9782052;
Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Engh R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6. MEDLINE-98421670; PubMed-9751050; Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Payletich N.P.; Structural basis for inhibition of the cyclin-dependent kinase Cdk6 by the tumour suppressor p161NK4a.";
                                                                                                     SEQUENCE FROM N.A.
MEDILTE=9636265; PubMed=8741839;
MEDILTE=96362665; PubMed=8741839;
Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Noh S., Wu X.,
Zariwala M., Matera A.G., Xiong Y.; Solation and characterization of pl9INK4d, a p16-related inhibitor specific to CDKG and CDK4.";
Mol. Biol. Cell 7:57-70(1996).
Lahti J.M., Sherr C.J., Downing J.R.; "Molecular cloning, expression pattern, and chromosomal localization of human CDKNZD/INK4d, an inhibitor of cyclin D-dependent kinases."; Genomics 29:623-630(1995).
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PDB; lbx.
MIN; 600927; ----
MIN; 600927; ----
MIN; 600927; ----
A InterFro; IPR002110; ANK.
JR Pfam; PF00023; ank; 3.
DR SMART; SM00348; ANK, 1.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT; 1.
The structure.

KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; 3D-structure.

A1 69 ANK 1.

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A1 1 69 ANK 2.

The structure and the structure and the structure and the structure.

A1 1 69 ANK 2.

ANK 4.
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Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                             Gaps
                                                                                                                                               4 SADWLATAAARGRVEEVRALL-EAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEP 62
                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-CS7BL KAPLAN;
MEDIINE-95257948; Pubbed-7739547;
Hiral H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;
Hiral H., Roussel M.F., Rato Jin, Ashmun R.A., Sherr C.J.;
Movel INK4 protebins, p19 and p18, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6.";
Mol. Cell. Biol. 15:2672-2681(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure of the cyclin-dependent kinase inhibitor p19Ink4d.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE-98013176; PubMed-9353127;
Luh F.Y., Archer S.J., Domaille P.J., Smith B.O., Owen D.,
Brotherton D.H., Raine A.R., Xu X., Brizuela L., Brenner S.L.,
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                                                                 Query Match

34.1%; Score 259; DB 1; Length 166;
Best Local Similarity 44.0%; Pred. No. 2.7e-18;
Matches 66; Conservative 18; Mismatches 60; Indels
Q -> P (IN REF. 3).
2FACD11CF56340DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      CDN7_MOUSE STANDARD; PRT; 166 AA.
060773; 060794;
01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
CDKN2D.
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                                                                                                                                                                                                                                                                                                    123 RAAAG----GTRGSNHARIDAAEGPSDIPD 148
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MEDLINE=95257949; Pubmed=7739548;
               17700 MW;
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EMBL; U20497; AAA85437.1; -.
PDB; 1AP7; 16-SEP-98.
                 166 AA;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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01-NOV-1997 (Rel. 35, Last sequence update)
20-NOC-2001 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6))
                   InterProf. 1PR00110; ANN.
ThresProf. 1PR00110; ANN.
SMART: SW00248; ANK. 1.
PROSITE; PS50088; ANK_REPEAT; 1.
Cell cycle; Anti-oncogene; Repeat; Ank_repeat; Anti-oncogene; Repeat; Ank_repeat; Ank_rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.8%; Score 249; DB 1; Length 16 ilarity 44.3%; Pred. No. 2.5e-17; Conservative 18; Mismatches 52; Indels
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ANK 3.

A -> P (IN REF. 2).

9E74F5C23B7EBCB2 CRC64;
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-!- SIMILARITY: CONTAINS 5 ANK REPEATS.
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138 166 AN
17 17 A
166 AA; 17894 MW;
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InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
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MGD; MGI:105387; Cdkn2d
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Best Local Similarity
Matches 70; Conserv
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SEQUENCE FROM N.A.
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CONFLICT
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CDN6_MOUSE
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X.*RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
MEDLINE=98100086; PubMed=9437433;
Venkataramani R., Swaminathan K., Marmorstein R.;
"Crystal structure of the CDK4/6 inhibitory protein pl8INK4c provides insights into ankyrin-like repeat structure/function and tumor-derived pl6INK4 mutations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Growth suppression by p18, a p16InK4/MTS1- and p14InK4B/MTS2-related CDK6 inhibitor, correlates with wild-type pRb function."; Genes Dev. 8:2939-2952(1994).
                                                                                                                                                                                                                                                                                                                                                                           PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARY 121
                                                                                                                                                                                                                                                    Gaps
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Blais A., Labrie Y., Pouliot F., Lachance Y., Labrie C.;
Structure of the gene encoding the human cyclin-dependent kinase
inhibitor p18 and mutational analysis in breast cancer.";
Biochem. Biophys. Res. Commun. 247:146-153(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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20-AUG-2001 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
KINASE 4 INHIBITOR C) (P18-INK4C).
CDKN2C OR CDKN6.
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MEDILIDE=95095079; PubMed-8001816;
Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Reefe C.L.,
Matera G.A., Xiong Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96438606; PubMed=8840966;
Lapointe J., Lachance Y., Labrie Y., Labrie C.;
"A p18 mutant defective in CDK6 binding in human breast cancer
                                                                                                                                                                                                                Length 168;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_raxID=9606;
                                                                                                                                                           BC88D5489307E128 CRC64;
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                                                                                                                                                                                                            30.5%; Score 231.5; DB 1;
40.3%; Pred. No. 1.3e-15;
live 22; Mismatches 60;
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SMART; SMO0248; ANK; 2.
PROSITE; PS50088; ANK_REPEAT; 2.
PROSITE; PS50297; ANK_REP_REGION; 1.
Cell cycle; Repeat; ANK repeat.
REPEAT 4 33 ANK 1.
                                                                  ANK 1.
ANK 2.
ANK 3.
ANK 4.
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LMKHTACNVGHRNHKGDTA 140
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102
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136
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Best Local Simi
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InterPro; IPR002110; ANK
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                                                                                                                                                                       -i- DISEASE: CDKN2C MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
                                                                                                          INHIBITS
                                                             Tumor suppressor INK4: determination of the solution structure of p18INK4C and demonstration of the functional significance of loops in p18INK4C and p16INK4A.";

p18INK4C and p16INK4A.";

p18INK4C and p16INK4A.";

c1. FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON ENDOGENOUR RETINOBLASTOMA POTEIN RB.

-1. SUBBURIT: HETERODIMER OF P18 WITH CDK6.

-1. TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN SKELETAL MUSCLE. ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARY 121
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PDB; 1...
PDB; 1...
RIM; 603369; ...
RIN; 603369; ...
REPEART; SM00248; ank; 4.
DR SMART; SM00248; ank; 2.
DR PROSITE; PS50039; ANK REP_REGION; 1.
ROSITE; PS50039; ANK REP_REGION; 1.
REPEART 4 33 ANK 1.
REPEART 7 4 33 ANK 1.
REPEART 7 65 ANK 1.
REPEART 7 65 ANK 1.
ANK 1.
ANK 2.
ANK 2.
ANK 2.
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ANK 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTId=VAR_001490.
5D66AFA715186E9A CRC64;
                                       Li J., Byeon I.-J.L., Ericson K., Poi M.-J., O'Maille Tsai M.-D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3924 AA.
                                                                                                                                                                                                         -! - SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                      EMBL, AF041248; AAC39782.1; --
EMBL, AF041249; AAC39783.1; --
EMBL, AF041249; AAC39783.1; --
PDB; 1HHB; 13-JAN-99.
PDB; 1BU9; 13-SEP-99.
MIM; 603369; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                  PubMed=10074345;
   Nat. Struct. Biol. 5:74-81(1998).
                                                                                                                                                                 FOUND IN PANCREAS AND HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 AA; 18127 MW;
                                                                                                                                                                                                                                                                                                                EMBL; U17074; AAC50074.1; -.
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                                  MEDLINE-99175088;
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Q01484; Q01485;
                                                                                                                                                                                                INHIBITORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIFFERENT PROTEIN KINASES THE PROTEIN'S STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                         Chan W., Kordeli E., Bennett V.; "440-kD ankyrinB: structure of the major developmentally regulated domain and selective localization in unmyelinated axons.";
                                                                                                                                                                                  Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E., Lux S.E., Ward D.C., Forget B.G.; "Isolation and chromosomal localization of a novel nonerythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Otto E., Kunimoto M., McLaughlin, T., Bennett V.;
"Isolation and characterization of cDNAs encoding human brain ankyrins reveal a family of alternatively spliced genes.";
J. Cell Biol. 114:241-253(1991).
01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID)
                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carpenter S.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: PHOSPHORYLATED AT MULTIPLE SITES BY
AND EACH PHOSPHORYLATION EVENT REGULATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
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SIMILARITY: CONTAINS 23 ANK REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell Biol. 123:1463-1473(1993).
                                                                                                                                                                                                                                                                                                                               TISSUE-Brain stem;
MEDLINE=94075409; PubMed=8253844;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain stem;
MEDLINE=91302466; PubMed=1830053;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                 TISSUE=Erythrocyte;

Machine = 2345717; Pubmed=1386265;

Mitch R.A. Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;

Muhite R.A. Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;

Muhite erythrocyte ankyrin cDNA: highly conserved regions of the
regulatory domain.";

Mamm. Genome 3:281-285(1992)

L. Fegulatory domain.";

Mamm. Genome 3:281-285(1992)

C. FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEIN GP85, AND TO THE
CYTOSKELETAL PROTEINS FODRIG, TUBULIN, VIMENTIN AND DESMIN.
CYTOSKELETAL PROTEINS FODRIG, TUBULIN, VIMENTIN AND DESMIN.
CYTOSKELETAL PROTEINS FODRIG, TUBULIN, VIMENTIN AND DESMIN.
CYTOSKELETAL PROTEINS FODRIG, TUBULIN, SPECTRIN (BETA CHAIN) TO THE
CYTOSKELETAL PROTEINS FODRIG, TUBULIN, SPECTRIN (BETA CHAIN) TO THE
CYTOSKELETAL PROTEINS FODRIG, TUBULIN, SPECTRIN (BETA CHAIN) TO THE
CYTOSKELETAL PROTEINS FODRIG, TUBULIN, SPECTRIN (BETA CHAIN)

CYTOSKELETAL PROTEINS FOOR THE CYTOSKELET S ANION EXCHANGE PROTEIN;

THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

CHI-CHAIN THEY RETAIN LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528 TNGYT-PLHISAREGQVDVASVLLEAGAAHSLATKKGFTPLHVAAKYGSLDVAKLLLQRR 586
                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 KDA REGULATORY DOMAIN (REGULATES THE BINDING OF ANKYRIN TO SPECTRIN AND THE BAND 3 PROTEIN).
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-i- PTM: ACYLARTED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
-i- SIMILARITY: CONTAINS 23 ANK REPEATS.
-i- SIMILARITY: CONTAINS I DEATH DOMAIN.
                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                               PRT; 1862 AA.
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                                                                                                                                                                                                    ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
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                                                                                                                               STANDARD;
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                             125 AAGGTRGSN 133
                                                        587 AAADSAGKN 595
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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MISSING (IN ISOPORM 2 AND ISOPORM 3).
GQ -> PE (IN REF. 4).
I -> S (IN REF. 2).

vv -> HA (IN REF. 2).
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-> Y (IN REF. 2).
52AC496C428E29D2 CRC64;
                                                                                                                                                         Cytoskeleton; Alternative splicing; Repeat; ANK repeat; Phosphorylation; Multigene family.
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                                                                                                              PROSITE; PS50088; ANK REPEAT; 20. PROSITE; PS50297; ANK REP_REGION; 1. PROSITE; PS50017; DEATH_DOMAIN; 1.
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InterPro; IPR000488; Death.
InterPro; IPR00906; 205.
Pfam; PF00023; ank; 24.
Pfam; PF00731; death; 1.
SMART; SM00248; ANK; 21.
SMART; SM00054; DEATH; 1.
SMART; SM00058; ZU5; 1.
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TISSUE-Hematopoietic;
MEDLINE-90158830; PubMed=2137557;
Lux S.E., John K.M., Bennett V.;
"Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQV-MMMGSARVÅELLLLHGAEPNCAD 66
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01-APR-1990 (Rel. 14, Last sequence update)
02-ABR-2001 (Rel. 40, Last annotation update)
ANKYRIN 1 (ERTHROCYTE ANKYRIN) (ANKYRIN S) (ANKYRINS 2.1 AND 2.2).
ANKI OR ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE-90175370; PubMed=1689849;
Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.6%; Score 133.5; DB 1; Length 768; 33.8%; Pred. No. 2.2e-05; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                   NK 14.
2913B69BE2DFE06D CRC64;
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                                                                                          InterPro; IPR02110; ANK.
Pfam: PF00023; ank; 13.
SMART; SM0248; ANK; 13.
PROSITE; P550088; ANK_REPEAT; 13.
PROSITE; P550297; ANK_REP_REGION; 1.
Hypothetical protein; Repeat; ANK repeat.
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ANK 3.
ANK 4.
ANK 5.
ANK 6.
ANK 7.
ANK 10.
ANK 11.
ANK 113.
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                                                             EMBL; AB033049; BAA86537.1; -. HSSP; P42771; 1BI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                   82819 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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44
82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                   416
768 AA;
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P16157;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DNA Res. 6:337-345(1999)
-:- SIMILARITY: CONTAINS AT LEAST 14 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQV-MMMGSARVAELLLLHGAEPNCAD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1862;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                        204242 MW; AE6B85B5B29001E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 18.1%; Score 137.5; DB 1;
L Similarity 34.7%; Pred. No. 2.4e-05;
51; Conservative 17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN KIAA1223 (FRAGMENT)
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626
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725
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                                                                                                                                                                                                                                                                                                                                                                                             AA;
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Best Local Similarity
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        TISSUE-Brain,
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DOMAIN
SEQUENCE
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YB23_HUMAN
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                                                         VARIANT HS ILE-462.

WEDLINE-96225450; PubMed-8640229;

WEDLINE-96225450; PubMed-8640229;

WEDLINE-96225450; PubMed-8640229;

BEDEY S.W., Gonzalez J.W., Lux M.L., Scarpa A.L., Tse W.T.,

Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,

Ankyrin-1 mutations are a major cause of dominant and recessive

The Ankyrin-1 mutations are a major cause of dominant and recessive

The Recitary spherocytosis. Paracel HINTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL

LI FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEIN GP85, AND TO

THE TO THE LYMPHOCYTE MEMBRANE PROTEIN BAND 4.2, TO

NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO

CYTOPLASMIC DOMAIN SPORTN, TUBULIN, VIREATIN AND DESMIN.

EXTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE

CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;

THEN ERYTHROCYTE CYTOPLASMIC SURFACE OF ERYTHROCYTIC

PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANYYRIN ARE PRODUCED BY ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANYYRIN
                                                                                                                                                                                                                                                                                                                                                                                           VARLANT 2.1.

-!- PTM: REGULATED BY PHOSPHORYLATION.
-!- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
-!- DISEASE: DEFECTS IN ANKI ARE THE CAUSE OF DOMINANT AND RECESSIVE HERBITARY SPHEROCYTOSIS (HS).
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55 KDA REGULATORY DOMAIN (REGULATES THE BINDING OF ANKYRIN TO SPECTRIN ANK 1.
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ANK 2.
ANK 3.
ANK 4.
ANK 5.
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BINDING DOMAIN).
62 KDA DOMAIN (SPECTRIN BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50088; ANK_REPEAT; 20.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
Phosphorylation; Lipoprotein; Multigene family; Disease mutation;
Elliptocytosis; Polymorphism.
Cheung M.C., Kan Y.W., Palek J.; "cDNA sequence for human erythrocyte ankyrin."; Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS 23 ANK REPEATS.
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002110; ANK.
InterPro; IPR000488; Death.
InterPro; IPR000906; ZU5.
Pfam; PF00023; ank; 23.
Pfam; PF00731; death; 1.
Pfam; PF00791; ZU5; 1.
SMART; SM0005; DEATH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X16609; CAA34610.1; -. EMBL; M28880; AAA51732.1; -.
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PIR; A35049; A35049.
HSSP; Q00420; IAWC.
MIM; 182900; -.
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ANK 6. ANK 7. ANK 9. ANK 10. ANK 11. ANK 11. ANK 11. ANK 12. ANK 13. ANK 13. ANK 14. ANK 14. ANK 15. ANK 19. ANK 19. ANK 19. ANK 20. ANK 20. ANK 21. ANK 21. ANK 21. ANK 21. ANK 21. ANK 22. ANK 22. ANK 23. ANK 23. BEATH. ANK 23. ANK 23. CINDEDPEREVOIPTENTRYEKER ANK 23. BEATH. ANK 23. ANK 23. CAPTICARCOOFS 2.2 MISSING (IN ISOFORM 2.2) FILIDAVAR_000595. V. > I (IN HS). /FTICAVAR_000596. R. > H (IN BRUEGGEN). /FTICAVAR_000597. V. > A. /FTICAVAR_000597. V. > A. /FTICAVAR_000599. E. > D. /FTICAVAR_000601. S. > T. /FTICAVAR_000601. S. > T. /FTICAVAR_000601. ANTICAVAR_000601. ANTICAVAR_000601. ANTICAVAR_000602. ANTICAVAR_000602. ANTICAVAR_000602. ANTICAVAR_000603. ANTICAVAR_006003.	Mismatches Mismatches NSTGREIV- TKKGFTPLHVA AGARLDVRDAW : GGSPHSPAW I 146 : M 649	PRT; 1431 AA. eated) st sequence update) st annotation update) KINASE 1 (EC 2.7.1)
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11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	52; Conservative TAARGRVEEVALLEA AAREGHVETVLALLEK I I I I I IAAREGTVETVLALLEK I I I I GLT-PLHVAVHHNNLDI -RAAAGGTRGSNHARID I I GLT-REVAVHARID -RAAAGGTRGSNHARID I I GLT-REVAVHARID -RAAAGGTRGSNHARID I I GLT-REVAVHARID	STANDARD; (Rel. 34, Cr. (Rel. 35, La. (Rel. 40, La. ATED PROTEIN
REPEAT RE	CChes 52; 8 LATAARE 8 LHIAARE 67 PATLIRE 566 KNGLT 123RAAA	RESULT 15 DAPK_HUMAN TD DAPK_HUMAN AC P53355, TO 10.0CT-1996 (Rel. DT 01.0CT-1997 (Rel. DT 20-AUG-2001 (Rel. DE DEATH-ASSOCIATED FGN DAPKI OR DAPK.
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Search completed: May 7, 2002, 12:36:42 Job time: 197 sec
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                                                                         SEQUENCE FROM N.A.
MEDLINE-95129831; Pubmed-7828849;
Delss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
"Identification of a novel serine/threonine kinase and a novel 15-kD protein as potential mediators of the gamma interferon-induced cell death.";
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                               Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase: Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis. DOMAIN 13 266 PROTEIN KINASE.
                                                                                                                                                                                                                                                     -i- PTM: AUTOPHOSPHORYLATED.
-i- SIMILARIY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-i- SIMILARIY: CONTAINS 10 ANK REPEATS.
-i- SIMILARIY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
K->A: LOSS OF ACTIVITY.
MW; 9EE84811004A155B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam: PF00023; ank; B.
Pfam: PF00023; ank; B.
Pfam: PF00021; death; 1.
Pfam: PF00069; pkinase; 1.
SMART: SM00248; ANK; T.
SMART: SM00205; DEATH; 1.
SMART: SM00200; DEATH; 1.
PROSITE: PS50089; ANK_REPEAT; 6.
PROSITE: PS50017; DEATH_DOMAIN; 1.
PROSITE: PS50017; PROTEIN_KINASE_ATP; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00109; PROTEIN_KINASE_ATP; 1.
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InterPro; IPR000488; Death.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_kin_actsite.
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REVISIONS TO 164-171.
Feinstein E.;
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1431 AA;
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HSSP; Qb.
TW: 600831;
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Score 130.5; DB 1; Length 1431;

17.28;

Query Match

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483 LHCAAWHGYYSVAKALCEAGCNVNIKNREGETP---LLTASARGYHDIVECLAEHGADLN 539
                    Gaps
                                                         8 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSAR----VAELLLLHGAEPN 63
                                                                                                                                     64 CADP-----TRPVHDAAREGFLDTLVVLHR 91
                  39;
                54; Indels
; Pred. No. 8.6e-05; 14; Mismatches 54
                                                                                                                                                                                                                   92 AGARLDVRDAWGRLPVDLAEELGHRDVARYL 122
                                                                                                                                                                                                                                         29.18;
Best Local Similarity 29.13
Matches 44; Conservative
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 7, 2002, 12:33:10; Search time 24.87 Seconds

(without alignments)

870.459 Million cell updates/sec

105-09-016-869B-35

Perfect score:
760
1 MEPSADWLATAAARGRVEBY......TRGSNHARIDAAEGPSDIPD 148

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries
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10: Sp_plant:*
11: Sp_rodent:*
12: Sp_virus:*
13: Sp_vertebrate:*
14: Sp_unclassified:*
Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:*

SPTREMBL_17:*

Database :

sp_organelle:* sp_phage:*

sp_mammal:*

sp_mhc:*

Result Query No. Score Match Length DB ID

1 548 72.1 106 4 Q9NPD5 Q9PQ5 D9PQ5 homo sapien Q9PQ3 G5.1 157 11 Q9PQ3 Q9PQ0 D9PQ0 D9PQ0

Oggwhd mus musculu P70067 xiphophorus Ogwel8 xiphophorus Ogdes6 fugu rubrip Ogdes3 fugu rubrip Ogdes3 fugu rubrip Ogdes3 fugu scabal Ogd153 mus musculu Og5440 homo sapien P97582 rattus norv Ognxy9 homo sapien Ogh2k2 homo sapien Ogh180 bos taurus Og109 mus musculu Oguqy1 homo sapien Ogb2171 homo sapien Ogb2171 homo sapien Ogb214 homo sapien Ogy213 mus spretus Ogh213 mus spretus Ogy213 mus spretus Ogy213 mus spretus Ogy213 mus spretus	Q13768 homo sapien Q99407 homo sapien Q9et47 mus musculu
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ALIGNMENTS

		-	(5)	(100)			ta; Euteleostomi;	dae; Homo.				hi K., Carson D.A.:	kinase-4 inhibitor gene in multiple								CRC64;		DB 4; Length 106; 1.8e-40; es 0; Indels 0; Gaps	43 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 102		IPD 148	
	PKT; IU6 AA.	Created)	Last sequence update)	arac amoracron abas	,		; Craniata; Vertebrata; Euteleostomi;				2487;	Nobori T., Miura K., Wu D.J., Lois A., Takabayashi K., Carson D.A.:	endent kinase-4 inhi				INED.		,	GION; 1.	; 2D59442F956B6A61 CRC64;		Score 548; Pred. No. 0; Mismatch	DPATLTRPVHDAAREGFLDT		GRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD	
. MAKETET TOOL	FRELIMINARI;	(TrEMBLrel.	0 (TrEMBLrel, 15,	IN (FRAGMENT)		ns (Human).	Eukaryota; Metazoa; Chordata;	<pre>Eutheria; Primates; =0606.</pre>		ROM N.A.	MEDLINE=94203288; PubMed=8152487;	Miura K., Wu D.J.	"Deletions of the cyclin-dependent	ers.";	Nature 368:753-756(1994).	24; AAD14050.1;	SOSBZZ; AADI4USU.1; JOINED.	InterPro; IPROUZIIU; ANK.	Figure Fronces; ank; 1.	PROSITE; PSSUZ9/; ANK_REP_REGION; I	106 AA; 11314 MW;	٠	72.1%; 100.0%; vative	SARVAELLLLHGAEPNCA	SARVAELLLHGAEPNCA	OLAEELGHRDVARYLRAA	
005 005 008 008 008	09NP05;	01-OCT-2000	01-OCT-2000 01-JUN-2001	CDK4I PROT	CDK4I.	Homo sapiens (Human)	Eukaryota;	Mammalia; Eutheria; NCBI TavID=0606.	[1]	SEQUENCE FROM N.A.	MEDLINE=94	Nobori T.,	"Deletions	numan cance	Nature 368	EMBL; S698;	EMBL; SOYB,	InterPro;	Fiall; Frunc	NON TEP	SEQUENCE		Query Match Best Local Similarity Matches 106; Conser	43 VMMMGS	1 VMMMGS	103 GRLPVI	
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Pred. No. 3.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                          121 YLRAAGNTPQGSEPAGVTSAQTP 143
                                                                                                                                                                                                                                                                                                                                                                                         121 YLRAAAGGTRGSNHARIDAAEGP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, p16 PROTEIN P16INK4A.
70.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 74.6
Matches 97; Conservative
                                    101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00023; ank; 4.
SMART; SM00248; ANK; 1
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   Best Local Similarity
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                                       Matches
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Q9R0Z3
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                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Muscarella P., Knobloch T.J., Weghorst C.M.;
Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and
"Sequencing of the Syrian Golden Alterations in Hamster Tumor Cell
Identification of Inactivating Alterations in Hamster Tumor Cell
                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLREL. 17, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR 2.
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Muscarella P., Knobloch T.J., Weghorst C.M.;
"Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and
Identification of Inactivating Alterations in Hamster Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 157;
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EMBL; AF291998; AAG59801.1; -.
EMBL; AF291997; AAG59801.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF292567; AAG44950.1; -
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
SWART; SM00248; ANK; 4.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLIN-DEPENDENT CELL CYCLE INHIBITOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 67.1%; Score 510; DB 11;
Local Similarity · 68.9%; Pred. No. 5.7e-37;
hes 102; Conservative 17; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 AA; 15206 MW; 8904F9C0C316A084
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                                                                               157 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Golden hamster)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                Mesocricetus.
NCBI_TaxID=10036;
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                                                                                   Q9EQ33
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P97510 P77510; P77510;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                     61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                           1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
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STRAIN=F344/N; TISSUE=LUNG;
MEDLINE=97184461; PubMed=9032263;
Swafford D.S., Middleton S.K., Palmisano W.A., Nikula K.J.,
Tesfaigzi J., Baylin S.B., Herman J.G., Belinsky S.A.;
"Frequent aberrant methylation of pl6INK4a in primary rat lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 159;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3C4CA920A1FEAEB6 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.7%; Score 476.5; DB 1:74.6%; Pred. No. 4.7e-34; ive 11; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 AA
     15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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EMBL: L81167; AAA48924.1; -.
HSSP: QG0773; 1AP7.
InterPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50297; ANK_REP_REGION; 1
SEQUENCE 159 AA; 17366 MW; 3C4C7
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Length 144;

DB 11;

Score 501;

65.98;

Query Match

5;

Length 168;

9A6B0F24F34D5FEC CRC64;

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62.4%; Score 474; DB 11; Length 168;
      17941 MW;
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      168 AA;
                                        Query Match
Best Local Similarity
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SEQUENCE 168
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                               66
      SEQUENCE
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C STRAIN-CAST/EI, C57BL/6J, ARF/J, AND MOLF/EI;
Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
Pellicer A., Fernandez-Piqueras J.;
T "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
I in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF044336, AAC008953.1;
R EMBL; U66087, AAB39600.1;
R EMBL; U66086, AAB39600.1;
R EMBL; U66086, AAB39600.1;
R EMBL; U660886, AAB39600.1;
R EMBL; U47018, AAAC32987.1;
R EMBL; U47018, AAAC32987.1;
R EMBL; U79628; AAB00226.1;
                                                                                                                                                                                                                                                                                                                                                                                         Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D., Richter K.H., Walker.C., Beach D., Sherr C.J., Serrano M.; "Cloning and characterization of murine pl6INK4a and pl5INK4b genes."; oncogene 11:635-645(1995)
                                                                                                                                                                                                                                "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor suppressor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soloff E.V., Herzog C.R., You M.; "The 5'-flanking region of the El alpha form of the murine pl6INK4a
             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                              STRAIN-DBA/ZN; TISSUE-SPLEEN;
MEDLINE-98151529; PubMed-9482902;
Zhang S., Ramsay E.S., Mock B.A.,
"CdKn2a, the cyclin-dependent kinase inhibitor encoding pl6INK4a.pl9ARF, is a candidate for the plasmacytoma susceptibility locus,
                                                                                                                                                                                                                                                                                                         Я.,
                                                                                                                                                                                                                                                                                                    Malumbres M., de Castro I., Santos J., Melendez B., Mangues
Serrano M., Pellicer A., Fernandez-Piqueras J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       [5]
SEQUENCE OF 1-42 FROW N.A.
STRAIN=DBA/2, AND C57BL/6;
Gressani K.M., Rollins L.A., Miller M.S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00248; ANK; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
Kinase; Cyclin.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-42 FROM N.A.
STRAIN=DBA/2, AND C57BL/6;
MEDLINE=95380169; PubMed=7651726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ICR SWISS;
MEDLINE=97128829; PubMed=8973369;
                                                                                                                                                                                                       MEDLINE-97179476; PubMed-9021155;
 Elalpha or P16INK4A.
                                                                                                                                                                                                                                                     Mamm. Genome 8:65-66(1997).
                                                                                                                                                                                                                                                                               SEQUENCE OF 1-155 FROM N.A.
                                                                                                                                                                                SEQUENCE OF 1-42 FROM N.A. STRAIN=VARIOUS STRAINS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-11 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U79625; AAD00223.1;
U79627; AAD00225.1;
P42771; 1BI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:104738; Cdkn2a.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MTS1) gene.";
Gene 180:213-215(1996).
                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J X DBA;
                                                                                                                                                                                                                      Herzog C.R., You M.;
                                                                     SEQUENCE FROM N.A.
 CDKN2A OR
                                                                                                                                 p19ARF,
Pctrl."
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Herzog C.R., You M.\,; "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
                                                                                                                                                                                                                 61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                 Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M., Pellicer A., Fernandez-Piqueras J.; "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; APO44335; AAC08962.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRATM=BALB/CANRT; TISSUE=SPLEEN;
MEDLINE=98151529; pubMed=482902;
Zhang S., Ramsay E.S., Mock B.A.;
"Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and p19ARF, is a candidate for the plasmacytoma susceptibility locus,
                                                            Gaps
                                                                                                               9
                                                                                                                                                                   9
                                                                                                                                         1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                            .,
8
                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
62.6%; Score 476; DB 11;
ilarity 63.9%; Pred. No. 5.5e-34;
Conservative 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                 121 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 147
                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-42 FROM N.A. STRAIN-BALB/CJ AND MUS MGS POSCHIAVINUS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MA/M4J;
MEDLINE=97179476; PubMed=9021155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U49279; AAC00051.1; -.
EMBL; U79855; AAD00224.1; -.
EMBSP; P55273; JBD8.
MGD; MGI:104738; Cdkn2a.
InterPro; IPR002110; ANK.
Ffan; PF00023; ank; 4.
SMART; SM00248; ANK; 1.
PROSITE; PS50297; ANK_REP_REGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suppressor gene.";
Mamm. Genome 8:65-66(1997).
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PRELIMINARY;
                                                                                                                                      103 1
103 AA;
SEQUENCE FROM N.A. STRAIN=LARGE WHITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9685;
                                                                                                                  Kinase; Cyclin.
NON_TER 103
SEQUENCE 103 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-PBMC;
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SEQUENCE
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           3
                                                                        61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                     Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y., Nishiqaki K., Watari T., Tsujimoto H., Hasegawa A.; "Cloning and chromosomal mapping of the feline genes pl6(MTS1/CDKNZA) and pl5(MTS2/CDKNZB)."; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; A2010807; BaA33540.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
            Gaps
                               1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGA 60
                                           1 VMMMGSARVAELLLLHGADPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 60
                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
P16/CDKN2A/MTS1 (FRAGMENT).
Fells slivestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9023;
[1]
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           8;
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Pred. No. 6.7e-32;
3; Mismatches 11; Indels
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          26399FF21359F35D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR, P16 (FRRGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 GRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 8.2e-34;
                                                                                                                                121 YLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 155
                                                                                                                  121 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 AA
                                                                                                                                                                                           102
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PROSITE; PS50297; ANK_REP_REGION; 1.
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                                                                                                                                                                                           PRT;
         17;
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86.0%;
63.28;
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Best Local Similarity 86.09
Watches 86; Conservative
           98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002110; ANK.
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                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   102
                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 AA;
Best Local Similarity
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. TISSUE=PBMC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                          09XS51
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         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 102
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Felis.
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Le Chalony C., Hayes H., Frelat G., Geffrotin C.; "Identification and mapping of swine CDKN2A and CDKN2B exon2
                                                                                                                                                                                                                                                                                                                      Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 86;
                                                                                                                                                                                                                                                                                                                    Score 444; DB 6; Length 10
Pred. No. 1.8e-31;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                              sequences.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJJ42787; CAB65454.1; -.
HSSP; P42771; 1B17.
                                                                                                                                                                                                                                                        5D23ABCC1088DE0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIS/WTS2/CDKN2B (FRAGMENT).

Pelis silvestris catus (Cat).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A59FF0193290E867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 GRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Pred. No. 4.5e-30;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 AA.
                                                                                                                      InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 2.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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11023 MW;
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Best Local Similarity 97.6%;
Matches 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.33
Matches 86; Conservative
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STRAIN=LARGE WHITE;
Le Chalony C., Hayes H., Frelat G., Geffrotin C.;
"Identification and mapping of swine CDKN2A and CDKN2B exon2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 408; DB 11; Length 86;
Pred. No. 2e-28;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U79639; AAD002341;
EMBL: U79638; AAD002331;
EMBL: U79638; AAD002331;
                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               509D9B3613251B18 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
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                                                                       103 GRLPVDLAEELGHRDVARYLRAAAG 127
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                                                                                            53.7%;
92.9%;
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9269 MW;
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Best Local Similarity 92.9°
Matches 79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinase; Cyclin.
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SEQUENCE
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                                                                                                                                                                                                                   Q9QUP0;
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"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: 079637; AAD00237.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus spretus (Western wild mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10096;
                                                                                                                     Canis familiaris (Dog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                                                                                                  Venkatraj V.S., Mayor J., Modiano J.F.;
"Role of pl6/Ink4 in familial canine cancers.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AF234176; AAG01087.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2090 (TrEMBLrel. 17, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 509D9B3613251B18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              0E39D8D805BEACOF CRC64;
                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLIN-DEPENDENT KINASE 4/6 INHIBITOR-A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 408; DB 11;
Pred. No. 2e-28;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 409; DB 6;
Pred. No. 1.5e-28;
0; Mismatches 1;
                      81 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002110; ANK.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                         PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                            81
8868 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                53.8%;
98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 53.7%;
Best Local Similarity 92.9%;
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                        InterPro; IPR002110; ANK
                                                                                                                                                                                                                                                                                                                                                                            81
81 AA;
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es 79; Conserv
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                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE
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0921C1;
                                                                                                                                                                                                                                                                                                                                               Kinase
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092121
002121
AC 092121
DT 01-MAX
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DT 01-JUN
DE CYCLIN
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CON MARMAN
OC BURARY
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OC BURARY
OC BURARY
OC STRATH
RP SEQUEN
RR SCOMPA
RR SUDMITTE
DR HSSP;
DR HSSP;
DR HSSP;
DR KINASE
RR KINASE
RR SUDMITTE
DR KINASE
RR KINASE
                       Q9GMF2
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43 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 102
                                                                                                                                                                                                                               STRAIN=VARIOUS STRAINS;
Santos J., Malundez B., Perez de Castro I., Malumbres M., Serrano M.,
Pellicer A., Fernandez-Piqueras J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Search completed: May
Job time: 193 sec
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NON_TER
SEQUENCE
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Matches
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                                                                                                                                                                                                      Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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0
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                                                                                                                                          Score 407; DB 6; Length 86;
Pred. No. 2.4e-28;
3; Mismatches 3; Indels
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ242788; CAB65455.1; -.
HSSP; P55273; LBD8.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 2.
PROSITE; P550297; ANK_REP_REGION; 1.
Kinase; CYCLIn.
1
SEQUENCE 86 AA; 9286 MW; 16EF7A223293CCF9 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malumbres M., Pellicer A.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AR015460; AAB94534.1; -.
HSSP: P55273; 1BDB.
Interpro; IRR002110; ANK.
PROSTIE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                             054846 PRELIMINARY; PRT; 86 AA.
054846.
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PISINK4B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 86 AA; 9237 MW; 0499DB26144FB6DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 405; DB 11;
Pred. No. 3.6e-28;
4; Mismatches 3;
                                                                                                                                                                                                                                          103 GRLPVDLAEELGHRDVARYLRAAAG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 GRLPVDLAEELGHRDVARYLRAAAG 127
                                                                                                                                                                                                                                                         61 GRLPVDLAEERGHRDVARFLRAAAG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus spretus (Western wild mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.3%;
91.8%;
                                                                                                                                          Query Match 53.6%;
Best Local Similarity 92.9%;
Matches 79; Conservative
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Best Local Similarity 91.83
Matches 78; Conservative
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Q9Z1C2;
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054846
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7, 2002, 12:36:23

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"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U79634; AAD00236.1; -.
HSSP; P55273; 1BD8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GRLPLDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Indels
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12073 MW; C3BFE8325DB2D79E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.9%; Score 334; DB 11;
61.1%; Pred. No. 7.1e-22;
tive 12; Mismatches 24;
                                                                                                                                                                                                                                                                                                Interpro; IPR00110; ANK.
Pfam; PF00023; ank; 2.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10096;
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113 AA;
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nes 69; Conserv
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(without alignments)
463.938 Million cell updates/sec
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1 MEPSADWLATAAARGRVEEV.....TRGSNHARIDAAEGPSDIPD 148
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Database :

A_Geneseq_1101:*

1. \SIDSB\gagdata/geneseq/geneseqp/AA1980.DAT:*
2. \SIDSB\gagdata/geneseq/geneseqp/AA1981.DAT:*
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14. \SIDSB\gagdata/geneseq/geneseqp/AA1991.DAT:*
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16. \SIDSB\gagdata/geneseq/geneseqp/AA1992.DAT:*
17. \SIDSB\gagdata/geneseq/geneseqp/AA1992.DAT:*
18. \SIDSB\gagdata/geneseq/geneseqp/AA1992.DAT:*
19. \SIDSB\gagdata/geneseq/geneseqp/AA1995.DAT:*
19. \SIDSB\gagdata/geneseq/geneseqp/AA1995.DAT:*
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20. \SIDSB\gagdata/geneseq/geneseqp/AA1999.DAT:*
21. \SIDSB\gagdata/geneseq/geneseqp/AA1999.DAT:*
22. \SIDSB\gagdata/geneseq/geneseqp/AA1999.DAT:*
22. \SIDSB\gagdata/geneseq/geneseqp/AA1999.DAT:*
22. \SIDSB\gagdata/geneseq/geneseqp/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Multiple tumour su	Human multiple tum	Inhibitor of cycli	Cell-cycle regulat	Human INK-4 protei	Human cell cycle r	CDK inhibitory fus	Human p27-p16 fusi	Human W3 protein s	Antiproliferative	Angiogenesis inhib
IES		_									
SUMMARIES	AAR81701	AAR80940	AAR53401	AAR85116	AAY24741	AAY88354	AAW23534	AAW95094	AAY97526	AAY96041	AAY96068
	16	16	15	16	20	21	18	20	21	21	21
% Query Match Length DB	148	148	151	156	156	156	391	391	391	391	391
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	760	760	760	760	160	760	160	760	760	160	260
Result No.	1	7	۳	4	S	9	7	ω	σ	10	11

Tumour suppressor Human multiple tum Amino acid sequenc Human maltiple tum Human multiple tum Human pl6 protein Human cyclin depen Human multiple tum Frotein encoded by Human Multiple Tum Human Multiple Tum Human Multiple Tum Human Multiple Tum Antiproliferative Angiogenesis inhib Truncated p27/pl6 Human W10 protein s Antiproliferative Angiogenesis inhib Secretable angiogenesis inhib Ch Inhibitory fus	assay; Osis;
•	MENTS polypeptide. lymphoma; progno
AMN10627 AMN19251 AMN40524 AMN40524 AMN60524 AMN5249 AMN50524 AMY20501 AMY9001	ALIGN (MTS1) MTS1; ca ukaemia;
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WPI; 1994-151320/18.
N-PSDB; AAQ63491.
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                                                                                                                                                                  148 AA;
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Matches 148;
                                                                                                                                                                  Sequence
                                                                                                                                                                                            Query Match
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                                                                     An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (WTS) gene, using gene probes which hybridise to the MTS1 gene ORF AAT00736 (which encodes AAR81701) mutant sequences AAT00749/50. The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
                                                                                                                                                                                                                                      Detecting polymorphism associated with cancer pre:disposition - also DNA, vectors and host cells e.g. for gene or protein replacement
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                     1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                               Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia; astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma; gene therapy; chronic.
                                                                                                                                                                                     ;
0
                                                                                                                                                                    Length 148;
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                                                                                                                                                                                                                                                                                                                                                                                        Human multiple tumour suppressor polypeptide, MTS1.
                                                                                                                                                                   100.0%; Score 760; DB 16;
100.0%; Pred. No. 4.4e-83;
ive 0; Mismatches 0;
                                                                                                                                                                                     0; Mismatches
                                                     Example 8; Pages 92-93; 148pp; English.
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94US-0214582.
94US-0215088.
94US-0227369.
94US-0215086.
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                                    therapy and drug screening
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                      Conservative
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N-PSDB; AAQ99158.
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Best Local Similarity
Matches 148; Conserv
                                                                                                                                           148 AA;
  N-PSDB; AAT00736.
                                                                                                                           cancers, etc..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994;
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61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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Wild-type multiple tumour suppressor (MTS) gene and mutant sequences - useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma or leukaemia
                                                                                                                                                                                         Several multiple tumour suppressor (MTS) polypeptides have been isolated and sequenced. This sequence is the MTS polypeptide MTSI MTS polypeptide modified MTSI mutants of these are useful for the diagnosis or prognosis of human cancer. Germ-line mutations of MTS cDNAs can be used for diagnosing predisposition to melanoma, leukaemia, astrocytoma, gliobastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild-type gene is useful for gene therapy and MTS polypeptides may also be used for protein replacement therapy. Also the polypeptides or cells contg. an altered MTS gene are useful for screening for potential cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclin; cyclin dependent kinase; CDK; oncogene; cancer; leukaemia; lymphoma; cell cycle; detection; identification; tumour virus; proliferating cell nuclear antigen; subunit; complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of subunit components of cyclin complexes - used for diagnosing transformation of a cell and developing inhibitors and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 148;
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100.0%; Pred. No. 4.4e-83;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                        Claim 5; Page 92-93; 156pp; English.
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us-09-016-869b-35.rag

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WPI; 1999-394656/33
                                N-PSDB; AAT02962
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18-NOV-1993;
14-APR-1994;
25-MAY-1994;
14-SEP-1994;
30-JUN-1995;
02-JAN-1996;
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                                                                                                                                                                                                                                             Sequence
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                                                The cell cycle gene implicated most strongly in oncogenesis is the human cyclin D1. It is genetically linked to the bcl-1 oncogene, a locus activated by translocation to an immunoslobulin gene enhancer in some B-cell lymphomas and leukaemias. D-type cyclin, cyclin dependant kinase (CDK), PCNA (proliferating cell nuclear antigen) and dependant kinase (CDK), PCNA (proliferating cell nuclear antigen) and combinatorial variations of the components e.g. cyclin D1 or D3 and CDK2, CDK4 and CDK5, assemble in vivo. Each quaternary complex may combinatorial variations of the components e.g. cyclin D1 or D3 and CDK2, CDK4 and CDK5, assemble in vivo. Each quaternary complex may types. Cellular transformation by DNA turnses such as SV40 is associated with selective subunit rearrangement of the cyclin D complexes. In virally transformed cells, CDK4 totally dissociates of from cyclin, PCNA and D21 and becomes associated with a 16 kilodalton polypeptide (p16). This sequence, designated pilonk4, binds to and inhibits CDK4. pl61NK4 was discovered to show many similarities to complex such as monoclonal antibodies, can be developed that recognise the interactions between the CDK's cyclins, PCNA and low molecular weight polypeptides and can therefore be used to identify the state of transformation of a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor; CCR; cancer; cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 760; DB 15; Length 151; 100.0%; Pred. No. 4.5e-83;
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 activators, partic for cancer treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beach DH, Demetrick DJ, Hannon GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell-cycle regulatory protein p16
                          Claim 13; Page 40; 45pp; English,
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94US-0227371.
94US-0248812.
94US-0306511.
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                                                                                                                                                                                                                                                                                                                                       151 AA;
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14-APR-1994;
25-MAY-1994;
14-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
                                                                          New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.
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transgenic mouse; p16-INK4-a; carcinogen; anti-proliferative.
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                                                                                                                                                                                 Claim 1; Page 76-77; 109pp; English.
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93US-0154915.
94US-0227371.
94US-0306511.
94US-0346147.
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WPI; 1995-373798/48.
                                                                                                                                                                                                                                                                                                                                                                                                                            156 AA;
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WPI; 2000-270336/23
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                    The present invention describes a transgenic mouse having germline and inhibits the ple-INK4-a gene leading to tumour susceptibility. Also described is a method of making a mouse and mouse embryonic stem cells a functionally disrupted pl6-INK4-a gene which comprises transferring a transgene construct into embryonic stem cells of a mouse and mouse and implanting these into a mouse blastocyst and implanting the resulting chimeric blastocyst into a female mouse selecting of spring having an endogenous pl6-INK4-a gene allele. The transgenic mouse is useful for evaluating the carcinogenic potential or the anti-proliferative activity of a test compound. The present sequence represents the human INK4 protein pl6 given in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                           Cell cycle regulatory protein; CCR; p16; diagnostic assay; detection; cell proliferation; differentiation; neoplasia; cancer; cell growth; cyclin-dependent kinase inhibitor; CDK; human; chromosome 9p21-22.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                             9 mepsadwlataaargrveevralleavalpnapnsygrrpiqvmmmgsarvaellllhga 68
                                                                                                                                                                                                                                                                                                                 1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                   Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cell cycle regulatory protein p16 amino acid sequence.
                                                                                                                                                                                                                                                                                         Indels
                       Transgenic mice with modified cell-cycle regulation
                                                                                                                                                                                                                                                                 100.0%; Score 760; DB 20;
100.0%; Pred. No. 4.7e-83;
ive 0; Mismatches 0;
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                                               Disclosure; Column 45-46; 35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                         121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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94US-0227371.
94US-0248812.
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95US-0497214
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                                                                                                                                                                                                                                156 AA;
 N-PSDB; AAX80472
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14-APR-1994;
25-MAY-1994;
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29-NOV-1994;
30-JUN-1995;
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                                                                                                                                                                                                                                Sequence
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This sequence represents the human cell cycle regulatory protein (CCR) pl6 amino acid sequence. The pl6 gene is located on chromosome 9p21-22. The invention relates to a diagnostic assay which comprises detecting a mutation in the pl6 gene, which is used to identify a cell or cells at risk of developing a disorder characterised by unwanted cell proliferation or differentiation. Pl6 is a cyclin-dependent kinase (CDK)-inhibitory protein, and functions as an inhibitor of cell-cycle projectsion and ultimately cell growth. The assay can be used for identifying a cell or cells at risk for a disorder (neoplasia) characterized by unwanted cell proliferation or differentiation. The method is used for detecting mutations in either a CCR gene or CDK gene which alter complex formation between these two proteins which is used for detecting mutations in other cellular proteins which also used for detecting mutations in other cellular proteins which other cellular proteins which disrupt binding of the psi protein with other cellular proteins, e.g. wilm's tumour suppressor protein with other cellular proteins, e.g. wilm's tumour suppressor protein with other cellular proteins such as ras protein or other cellular proteins which interact with mas as grease activating proteins (GAPS). The method is convenient for detecting mutants of CCR genes encoding proteins which are unable to physically interact with a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                      Use of a mammalian cell cycle regulatory protein (a CDK-inhibitory protein) in a diagnostic assay for identifying a cell at risk for a disorder characterized by unwanted cell proliferation or
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4.7e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 760; 100.0%; Pred. No. 4
                                                                                                                                                                                                             Claim 14; Column 57-58; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 ylraaaaggtrgsnharidaaegpsdipd 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "poly-His tag"
Misc-difference 205..219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes encoding procession.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
N-PSDB; AAA13096
                                                                                                                                                          differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
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This sequence represents a chimeric polypeptide of the invention. It was derived from a fusion of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the livention have cyclin-dependent kinase (CDK) binding motifs from at least two different proteins that bind to CDKS.

The protein controls proliferation and/or differentiation of cells, carticularly they inhibit cell-cycle progression. They can be used to treat a wide range of proliferative disorders, e.g. cancer, leukaemia, psoriasis, atherosclerosis, restencosis, chronic inflammation etc. They can also treat diseases associated with de-differentiation or degeneration of tissue, e.g. Alzheimer's, parkinson's or Huntington's diseases, gastric ulcers and autonomous diseases of the peripheral nervous system. Other applications include reducing growth of hair and protecting hair follicle cells against cytotoxic treatments, cosmetically to treat various forms of folliculitis, and to inhibit spermatogenesis or cogenesis. The chimeric proteins can also be used in vitro to maintain compensation inhibit can binding motifs used more active inhibitors of the CDK/cyclin complex than binding motifs used the coll colliculation in the cell cycle. The proteins are more active inhibitors of the CDK/cyclin complex than binding motifs used the coll colliculation in different stages of the coll colliculation.
                                                                                                                                                                                                                                                                                                                                                                          Chimeric inhibitor of cyclin dependent kinase - useful for gene therapy of cancer and other proliferative and differentiative
  /note= "(Gly4Ser)2 linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 40; Page 38-40; 58pp; English.
                                                                                                                                                                                                                                                                Gyuris J, Lamphere L;
                                                                                                                                                                           96US-0589981.
                                                                                                                                97WO-US00569
                                                                                                                                                                                                                     (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                            WPI; 1997-393685/36.
                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT74051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the cell cycle)
                                           WO9727297-A1
                                                                                                                                17-JAN-1997;
                                                                                                                                                                           23-JAN-1996;
                                                                                       31-JUL-1997
                                                                                                                                                                                                                                                                Beach D,
                                                                                                                                                                                                                                                                                                                                                                                                                     diseases
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0; Gaps 100.0%; Score 760; DB 18; Length 391; 100.0%; Pred. No. 1.6e-82; Indels . 0 Mismatches · 0 Conservative Similarity Matches 148; Query Match Best Local

391 AA;

Sequence

; 0

1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60 a a δ

61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120 ŏ g

121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148 364 ylraaaggtrgsnharidaaegpsdipd 391 δŽ qq

AAW95094

AAW95094 standard; Protein; 391 AA.

AAW95094;

(first entry) 25-MAY-1999 EX TX XX BE

Human p27-p16 fusion protein.

Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16

Homo sapiens.

W09906540-AZ.

11-FEB-1999.

98WO-US15759. 29-JUL-1998; 97us-0902572. 29-JUL-1997;

(MITO-) MITOTIX INC.

Lamphere L; Gyuris J, Beach DH,

WPI; 1999-153770/13. N-PSDB; AAX26220. Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers, fibrosis and neurodegeneration

Claim 63; Page 70-72; 88pp; English.

CUDKS), particularly CDK/cyclin complexes. It proyides a recombinant transfection system (A) that comprises: (i) first gene construct comprises: (i) first gene construct transfection system (A) that comprises: (i) first gene construct comprising a sequence encoding an inhibitory polypeptide contraining at last one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (ii) second gene construct comprising a sequence ehocding a polypeptide that promotes endothalialsation, and (iii) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (i) a therapeutic polypeptide sequence (TP) from an intracellular protein that alters a cellular process when FP enters the cell, and (ii) a transcellular process when FP enters the cell, and (ii) a transcellular process when FP enters the cell, and (ii) a transcellular process when FP enters the cell, and (ii) a transcellular process when FP enters the cell, and (ii) a transcellular process when FP enters the cell, and (ii) a transcellular process when FP enters the cell, and (ii) a transcellular process when FP enters the cell, and (ii) a transcellular wounds that involve a break in the endothelium and excessive proliferation of smooth muscale, particularly restenosis but more generally any repeal of cardiovascular damage, arteriosclerotic lesions or for endothelialisation of synthetic vascular grafts. More generally, FP are used to treat unwanted cellular proliferation in eurodegeneration in a very wide range of struations, e.g. for treating vascular diseases as above; fibrotic disorders (e.g. rheumatoid arthritis, diabetes, cirrhosis); many cumours (gliomas, leukaemias); chronic inflammation; neurodegeneration; cenes; also to control hair growth (e.g. to prevent hair loss caused by chemical control hair growth (e.g. to prevent hair loss caused by the part of the part of the part of the part of the part o to inhibit spermatogenesis etc. Chimmeric proteins comprising CDK-binding motifs from two or more different proteins bind to CDKs so inhibit cell cycle progression, particularly smooth muscle cell proliferation. The gene constructs may also be used to produce FP in cell cultures, for production or for regulating cell differentiation in vitro. The present The invention relates to novel inhibitors of cyclin-dependent kinases sequence represents a human p27-p16 fusion protein.

391 AA; Sequence

ö Gaps ; Length 391; Indels 100.0%; Score 760; DB 20; 100.0%; Pred. No. 1.6e-82; ; 0 Mismatches ; 0 Matches 148; Conservative Local Similarity Query Match

1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60

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us-09-016-869b-35.rag

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304 epncadpat1trpvhdaaregf1dt1vv1hragar1dvrdawgr1pvd1aee1ghrdvar 363
                                                                                                                                                                                                                                     Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; p27; INK4; p16; human; smooth muscle cell; hyperproliferation; restenosis; vasotropic; antiproliferative; gene therapy.
                                                                                                                                                                                                            Antiproliferative p27-p16 fusion protein W3.
                          AAY96041 standard; Protein; 391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2000; 2000WO-US04971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CELL-) CELL GENESYS INC. (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200052159-A1.
                                                                                                                                                                                                                                                                                              Homo sapiens.
Synthetic.
                                                                                                                                                                                 05-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mcarthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-2000
                                                                                                                                                     AAY96041;
                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                       364
                             121
                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                              AAY96041
                                                       qq
                                                                                                                                                        a
                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the human W3 protein.

The invention relates to a protein composition comprising a novel purified chimeric cyclin dependent kinase inhibitor (CDK1) and a purified adenovirus E4 protein. The compositions comprising the protein, or the DNA encoding it are useful for treating neoplasias in animals. The compositions also find use in assays to eliminate a specific sub-population of cultured cells, to determine the susceptibility of neoplastic cells to treatment with the compositions and also in assays to synchronise cell growth in cultured cells.
244 mepsadwlataaargrveevralleavalpnapnsygrrpiqvmmmgsarvaellllhga 303
                                        Protein and nucleic acid compositions for preventing and treating neoplasias (particularly cancer), comprises a novel chimeric cyclin dependent kinase inhibitor and adenovirus E4 protein -
                           61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR
                                                                                                                                                                                                                                                                                           Human; chimeric cyclin dependent kinase inhibitor; CDKi; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Finer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 760; DB 21;
Pred, No. 1.6e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mendez MJ,
                                                                                                                                                                                                                                                                                                         adenovirus E4 protein; neoplasia; W3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 108-109; 126pp; English.
                                                                               121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                               AAY97526 standard; Protein; 391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gyuris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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99US-0128271.
99US-0128515.
                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2000; 2000WG-US05350
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                 Human W3 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENESYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patel S, McArthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-587315/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOTIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 AA;
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                                                                                                                                                                                                                                                                                                                                                                 WO200052184-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1999;
08-APR-1999;
09-APR-1999;
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELL
                                                                                                                                                                                                                                    15-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-2000.
                                                                                                                                                                                                           AAY97526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CELL-)
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Location/Qualifiers

(first entry)

/label= 6His_tag

/label= p27

/label= Hinge 239..391 /label= p16

99US-0122974 99US-0163682 99US-0457568

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Novel recombinant lentivirus for inhibiting proliferation of smooth muscle cells in e.g. restenosis, is replication deficient and comprises a transgene encoding a cyclin dependent kinase inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of p27-p16 fusion protein W3 comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eland E4 regions, and comprises a transgene encoding a cyclin dependent kinase inhibitor (CDKi). The CDKi is selected from an INK4 family protein such as human pl6, a CIP/KIP family protein such as man pl6, a CIP/KIP family protein comprising (active fragments of these, or fusion proteins comprising (active fragments of) an INK4 family protein and a CIP/KIP family protein (see AAY96046 and AAY96049). The method is uto inhibit mammalian smooth muscle cell hyperprollferation, induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an N-terminal 6His tag, the human p27 protein (see AAY96052), a Clq4Ser)3 Hinge and the human p16 protein (see AAY96053). It is encoded by a nucleic acid obtained by PCR amplification of p27 and p16 DNAs using primers that also included codons for the tag/hinge regions. A claimed method for inhibiting smooth muscle cell hyperproliferation involves transducing smooth muscle cells with a replication-deficient recombinant adenovirus that lacks functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 101-103; 126pp; English.
Finer M;
Gyuris J,
                                                                                            WPI; 2000-594183/56.
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Gaps

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Indels

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Mismatches

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Conservative

148;

Matches

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Local Similarity

61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120

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WO9703635-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                 progression.
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                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-FEB-1997.
                                                                                                                                                                                                                 Seguence
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                                                                                                                   Gaps
                                                                                                 1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
by injury caused by angioplasty, stent placement or vein engraftment. It is useful for treating vascular pathologies e.g., restenosis. Also claimed are recombinant lentiviruses encoding
                                                                                                                                                                                                                                                                      human; anglogenesis; inhibitor; neoplasia; rheumatoid arthritis; endometriosis; psoriasis; vascular retinopathy; oytostatic; antiarthritic; antirheumatic; gynaecological; antipsoriatic;
                                                                            ;
0
                                                                                                                                                                                                                                                                Cyclin dependent kinase inhibitor; CDKi; CIP; KIP; INK4; p27;
                                                            Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inhibiting angiogenesis and treating angiogenesis-associated
                                                                           Indels
                                                           100.0%; Score 760; DB 21;
100.0%; Pred. No. 1.6e-82;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                 Anglogenesis inhibitor (p27-p16 fusion) W3.
                                                                                                                                                          121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                     AAY96068 standard; Protein; 391 AA.
                                                                                                                                                                                                                                                                                                                                               /label= 6His_tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŗ,
                                                                                                                                                                                                                                                                                              antiproliferative; gene therapy
                                                                                                                                                                                                                                                                                                                                                       8..204
/label= p27
205..219
/label= Hinge
239..391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0122974.
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99US-0457646.
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                                                                                                                                                                                                                                                                                                                                                                                            /label= p16
                                                                                                                                                                                                                                  05-DEC-2000 (first entry)
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CELL-) CELL GENESYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patel S, Mcarthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-565501/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MITO-) MITOTIX INC
                                                                   Similarity
                                     391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA50523
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                                                                                                                                                                                                                                                                                                            Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-1999;
09-DEC-1999;
                                                           Query Match
Best Local Simi
Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                         08-SEP-2000
                                     Sequence
                                                                                                                                                                                                                    AAY96068;
                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                        Protein
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The present sequence is that of p27-p16 fusion protein W3

comprising an N-terminal 6His tag, the human p27 protein (see
AAY96067). The fusion protein is encoded by a nucleic acid (see
AAA50523) that was obtained by PCR amplification of human p27 and p16
DNAS using primers that also included codons encoding the tag/hinge
regions of the fusion protein. A claimed method for inhibiting
regions of the fusion protein. A claimed method for inhibiting
transgene encoding a cell dependent kinase inhibitor (CDKi). The
delivery system for the transgene is a liposome or a recombinant
of the invery system for the transgene is a liposome or a recombinant
of the invery system for the transgene is a liposome or a recombinant
of the invery system for the transgene is a liposome or a recombinant
of the inverse is a protein of the CIP/KIP family such as p27, a
protein of the INK4 family such as p16, active fragments of these
proteins or a fusion of 2 CDKi proteins such as p27 and p16. The
method is useful in treating conditions associated with angiogenesis,
such as neoplasia, rheumatoid arthritis, endometriosis, psoriasis
and vascular retinopathy (claimed). Alternatively, the transgene
c such that the CDK1 is released into the blood and contacts the
target epithelial cell. The p27-p16 fusion proteins interact with
cCDK4/cyclinb, CDK2/cyclinA and CDK2/cyclinE and inhibit cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4; cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy; anti-angiogenic activity; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDÄWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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conditions, e.g. neoplasia, psoriasis by transducing an endothelial cell with a recombinant virus having a transgene encoding a cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                           Example 1; Page 108-110; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW10627 standard; Protein; 156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0502881.
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                                                                                  dependent kinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour suppressor p16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391 AA;
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Skolnick MH;

Kamb A,

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94US-0227369.
                       95WO-US03537
                                                (MYRI-) MYRIAD GENETICS INC
                                                          (UTAH ) UNIV UTAH RES FOUND
                                                                                   Cannon-Albright LA,
                                                                                                          WPI; 1997-258217/23.
                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                       N-PSDB; AAT72311
                                                                                                                                                                                                                                               156
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18-MAR-1994;
18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
14-APR-1994;
01-JUN-1994;
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17-MAR-1995;
                        17-MAR-1995;
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                                                                                                                                                                                                                                                                                                          Matches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-APR-1994
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW74549;
                                                                                                                                                                                                                                                                                   Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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                                                                                                                                           This sequence represents the tumour suppressor p16. The DNA encoding this sequence is joined to a promoter functional in eukaryotic cells and used in the expression construct of the invention. P16 is an inhibitory subunit, which is involved in the control of cyclin-dependent kinase 4 activity, and functions as a tumour suppressor. By detecting this sequence or the DNA encoding it, cancer cells can be detected. When the construct can be used to restore p16 function in a cell, particularly by reversing the transformed phenotype in tumours, especially lung or reversing the transformed phenotype in tumours, especially lung or construct can melanoma. It may also have anti-angiogenic activity, and inhibit hyperproliferative disorders, e.g. restenosis. When the nucleic acid molecule is inserted in the antisense orientation, the capression construct inhibits p16 function. Reduced or increased levels of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EPNCADPATLIRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 mepsadwlataaargrveevralleagalpnapnsygrrpigvmmmgsarvaelllhga 68
                                                                       Expression construct contg. DNA for tumour suppressor p16 - to restore p16 activity to transformed cells, useful for treating lung or bladder cancer or melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
                                                                                                                                                                                                                                                                                                                                                                                                                    ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                             Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Score 753; DB 18;
Pred. No. 3.3e-82;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human multiple tumour suppressor 1 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW19251 standard; Protein; 156 AA.
                                                                                                                         Disclosure; Fig 1b; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.3%;
Matches 147; Conservative 0
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94US-0214582.
94US-0215086.
94US-0215087.
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                                     WPI; 1997-132336/12
                                                                                                                                                                                                                                                                                                                                                            156 AA;
                                                 N-PSDB; AAT60951
               Roth J;
                                                                                                                                                                                                                                                                                                                                      or immunoassay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-1997
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18-MAR-1994;
18-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                            Sequence
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               Jin X,
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61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
                                                                                                                                                                                                                                                                                                             1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
                                                                                                                                                                                                                                                                                                                                     .;
0
Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s)
                                                                                                                                                                                                                             Length 156;
                                                                                                   The present sequence the human multiple tumour suppressor 1 (MTS1) gene product, useful in cancer diagnosis.
                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of multiple tumour suppressor 1.
                                                                                                                                                                                                                             Score 753; DB 18;
Pred. No. 3.3e-82;
0; Mismatches 1;
                                                              Claim 1; Columns 61-64; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW74549 standard; Protein; 156 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 somatic mutation; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        940S-0214582.
940S-0215086.
940S-0215087.
940S-0227369.
940S-0251938.
                                                                                                                                                                                                                               99.18;
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Sequence
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                        Kamb A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation; familial melanoma locus; MLM; predisposition.
                                                                                                                                                                        This is the amino acid sequence of the multiple tumour suppressor I (MTS-1) protein, used in the method of the invention. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein minetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used to restore MTS function in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPNCADPATLIRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 753; DB 19; Length 156;
Pred. No. 3.3e-82;
0; Mismatches 1; Indels
                                                                                                                                            Disclosure; Column 63-64; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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94US-0214582.
94US-0215086.
94US-0227369.
94US-0227369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.1%;
Best Local Similarity 99.3%;
Matches 147; Conservative
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WPI; 1998-494842/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MTS1 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                   156 AA;
                  N-PSDB; AAV53819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
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                                                                                                          mutation(s)
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This sequence represents a human multiple tumour suppression protein, MTS1. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 156;
                                                                                  DNA specific for Multiple Tumour Suppressor 1E1-beta gene useful for the diagnosis of cancers related to MTS1E1-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.1%; Score 753; DB 19; 99.3%; Pred. No. 3.3e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                   Disclosure; Column 63-64; 72pp; English.
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Job time: 555 sec
                                                                                                                                            mutation(s) and their treatment
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Matches 147; Conservative
WPI; 1998-250421/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                           N-PSDB; AAV11238
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RESULT 1
PCT-US95-03316-2
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                                                                                                                                                                                                                    7, 2002, 12:32:10 ; Search time 105.99 Seconds (without alignments) 490.476 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEPSADWLATAAARGRVEEV.....TRGSNHARIDAAEGPSDIPD 148
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... / cgn2_6/ptodata/2/paa/US084_cOMB.pep:*
... / cgn2_6/ptodata/2/paa/US082_cOMB.pep:*
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... / cgn2_6/ptodata/2/paa/US092_cOMB.pep:*
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/cgn2_6/ptodata/2/paa/USO7_MERGED_COMB.pepl:*
/cgn2_6/ptodata/2/paa/USO6_MERGED_COMB.pepl:*
/cgn2_6/ptodata/2/paa/PCT_MERGED_COMB.pepl:*
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6/ptodata/2/paa/US09_MERGED_COMB.pep1:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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1. /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
22. /cgn2_6/ptodata/2/paa/USO6_COMB.pep:*
3. /cgn2_6/ptodata/2/paa/USO7_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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                                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                    Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Ouery No. Score Match Length DB ID Description
1 760 100.0 148 1 PCT-US95-03316-2 Sequence 2, Appli
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PCT-US95-03537-2 US-08-214-581-2 US-08-214-582-2 US-08-215-086-2 US-08-215-087-2 US-08-227-369-2 US-08-227-369-2 US-08-227-311-2	2 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 - 0 -	US-09-016-537 US-09-016-537 US-09-016-750 US-09-016-750 US-09-016-869 US-09-016-869 US-09-016-869 US-09-016-869 US-09-016-869 US-09-016-869 US-09-016-869 US-09-016-869 US-09-016-018-018-018-018-018-018-018-018-018-018	08 474 - 083 - 08 - 479 - 083 - 08 - 479 - 731 - 08 - 502 - 881 - 09 - 0272 - 233 - 09 - 457 - 646 - 09 - 516 - 065 - 09 - 614 - 099 - 09 - 09 - 614 - 099 - 09 - 09 - 614 - 099 - 09 - 09 - 09 - 09 - 09 - 09 -
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ALIGNMENTS

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Sequence 2, Application PC/TUS9503316
GENERAL INFORMATION:
APPLICANT: Ramb, Alexander
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: MTS GENE, SOMATIC MUTATIONS IN THE MTS
TITLE OF INVENTION: GENE, AND METHODS FOR DIAGNOSIS, PROGNOSIS AND THERAPY OF
TITLE OF INVENTION: CANCER DUE TO THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESSONDENCES: 36
CORRESSONDENCES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STREET: 1201 New York Avenue, Suite 1000
STRYE: DC
COUNTRY: USA
ZIP: 2006
STRYE: FILMP PC Compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACEARIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: PCT/US95/03316
FILING DATE:
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SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,581
APPLICATION NUMBER: PCT/US95/03537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-03537-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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Matches 148; Conserve
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APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.30
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100.0%; Score 760; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                24884-109348-PCT-2
                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-0104-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,088
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,581
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9503537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 38,609
REGISTRATION NUMBER: 246
REFERENCE/POCKET UNBER: 246
TELECOMMUNICATION: TELECHONE: 202-962-4848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein PCT-US95-03316-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
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PCT-US95-03537-2
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61 EPNCADPATLIRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08214581
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: METHOD FOR THERAPY OF CANCER DUE TO
TITLE OF INVENTION: THE MTS GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: venable, Baetjer, Howard & Civiletti STREET: 1201 New York Avenue, Suite 1000 CITY: Washington STATE: DC COUNTRY: USA ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24884-109348-PCT-1
                                                                                                                                                                                                                                     FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 34,684-10934
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Gaps

us-09-016-869b-35.rapm

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61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                        Length 148;
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                                                               Indels
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GENERAL INFORMATION:
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, Suite 1000
                      100.0%; Score 760; DB 6;
100.0%; Pred. No. 1.4e-75;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 760; DB 6; Best Local Similarity 100.0%; Pred. No. 1.4e-75; Matches 148; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24884-109348
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18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
RECISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 148 amino acids
amino acid
                                          Best Local Similarity 100.0
Matches 148; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-215-086-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                        Length 148;
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GENERAL INFORMATION:
APPLICANT: Kanb, Alexander
TITLE OF INVENTION: SOMATIC MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 760; DB 6;
100.0%; Pred. No. 1.4e-75;
tive 0; Mismatches 0;
                CLASSIFICATION: 800
ATTONREY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFRERENCE/CDCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPRAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,582
CLIASIFCATION: 435
ATTORNEY/AGENT INRORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                 LENGTH: 148 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202-962-4810
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Best Local Similarity 100.(
Matches 148; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-214-581-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-214-582-2
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US-08-214-582-2
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                    CITY: Wa
STATE: D
COUNTRY:
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Sequence 2, Application US/08215087
GENERAL INDORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO TITLE OF INVENTION: AT THE MTS GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 148;
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GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND PROGNOSIS OF
TITLE OF INVENTION: CANCER DUE TO THE MTS GENE
TUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venable, Baetjer, Howard & Civiletti
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100.0%; Pred. No. 1.4e-75;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOGTWARE: WAND PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,087
FILING DATE: 18 -MAR 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-8100
121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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LENGTH: 148 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.(
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-215-087-2
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COUNTRY:
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US-08-215-088-2
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61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 760; DB 6; Length 148; 100.0%; Pred. No. 1.4e-75;
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GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: SOMATIC MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                  FILING DATE: 18-MAR-1994
CLASSIFFCATION: 436
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PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
                                                                               ZIP: 2005
ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,088
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,369
FILING DATE: 14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                             CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 148 amino acids
amino acid
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Best Local Similarity 100.0
Matches 148; Conservative
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Sequence 16, Application US/09480135
GENERAL INFORMATION:
APPLICANT: Shorr Ph.D., Charles J.
APPLICANT: Shorr Ph.D., James
APPLICANT: Hirai Ph.D., Hiroshi
APPLICANT: Hirai Ph.D., Hiroshi
APPLICANT: Hirai Ph.D., Hiroshi
APPLICANT: Oxida, Tsukasa
TITLE OF INVENTION: Cyclin Dependent Kinases GDK4 and CDK6, and Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX PLLC
                                                                                                                                                                                                                                                                                                                                                                                            1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGA 60
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                                                                                                                                        Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: STERNE, KESSLER, GOLDSTEIN & FOX PLLC 1100 New York Ave., Suite 600, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/480,135
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                                                                                                                                 100.0%; Score 760; DB 6;
ilarity 100.0%; Pred. No. 1.4e-75;
Conservative 0; Mismatches 0;
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APPLICATION NUMBER: 08/384,106
FILING DATE: 06-FEB-1995
ATTORNEY/ACENT INFORMATION:
NAME: FOX, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 16:
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                 protein
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Best Local Similarity
Matches 148; Conserv
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          ; MOLECULE TYPE:
US-08-227-371-2
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COUNTRY: US
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US-09-480-135-16
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                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatry Protein, and Uses
TITLE OF INVENTION: Cell-Cycle Applicant Collection C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 760; DB 6;
nilarity 100.0%; Pred. No. 1.4e-75;
Conservative 0; Mismatches 0;
                                                                                                                                 24884-109348
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,371
FILING DATE: 14-APR-1994
CLASSIETCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSI-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREFT: LAHIVE & COCKFIELD STREFT: 60 State Street CITY: Boston TAFF: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION UNDBER: 36,705
REFERENCE/DOCKET NUMBER: CSI-C
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.,
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2488:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-962-4810
TELEFAX: 202-962-4810
                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 148 amino acids
                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-227-369-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
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Best Local Similarity
Matches 148; Conserv
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US-08-227-371-2
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121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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                                                                                                                                                                                                                                                                                                                                            STATE: MA
COUNTRY: USA
ZIP: 02110
                                                                           US-09-016-869B-35
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                                                                                                                                                                                                                                                              Sequence 24, Application US/09480135
GENERAL INFORMATION:
APPLICANT: Sherr Ph.D., Charles J.
APPLICANT: Downing M.D., James
APPLICANT: Hiral Ph.D., Hiroshi
APPLICANT: HIRAL Ph.D., Hiroshi
APPLICANT: Nowda, Tsukasa
TITLE OF INVENTION: InK4c-pl8 and InK4d-Pl9, Inhibitors of
TITLE OF INVENTION: 2yclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                           61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOLDSTEIN & FOX PLLC Suite 600, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/480,135
FILING DATE: Herewith
CLASCIPTATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 760; DB 18;
100.0%; Pred. No. 1.4e-75;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0656.0500002
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                                                                                                                                       121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                           121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION WHMBER: 08/384,106
FILING DATE: 06-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30,353
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 148 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: STERNE, KESSLER,
1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
STREET: 11
                                                                                                                                                                                                                                    RESULT 11
US-09-480-135-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-480-135-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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EPNCADPATLTREVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLEVDLAEELGHRDVAR 120
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                                                 APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
TITLE OF INVENTION: Uses Related Thereto
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 148; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: GPCI-P10-071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 951-7739
TELEFAX: (617) 951-7739
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION UNDERS.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/893,274
FILING DATE: 15-UUL-1994
PRIOR APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-194
PRIOR APPLICATION NUMBER: US 08/206,511
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-DEC-1992
ATTORNEY APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY AMENT: NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,869B
FILING DATE: 30-JAN-1998
                                                                                                                                                                                                                                                                     ADDRESSEE: Ropes & Gray
STREET: One International Place
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 35, Application US/09016869B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 148 amino acids
amino acid
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ZIP: 02109
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                                                                                                                                                                                               STATE: M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMGSARVAELLLLHGA 68
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                                                                                                                                                                                          APPLICANT: Beach. David H.
APPLICANT: Beach. David H.
APPLICANT: Beach.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
APPLICANT: Quelle, Dawn E.
APPLICANT: Sherr, Charles J.
APPLICANT: OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 4
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 760; DB 6; Length 156; Best Local Similarity 100.0%; Pred. No. 1.5e-75; Matches 148; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFO 530

NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-594
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 antito acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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                                                        121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,812
FILING DATE: 25-WAY-1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                         STREET: 60 State Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/08306511; GENERAL INFORMATION:
                                                                                                                                                         Sequence 2, Application US/08248812 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-248-812-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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US-08-306-511-2
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                                                                                                                                             US-08-248-812-2
                                                                                                                          RESULT 13
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61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGA 60
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses
TITLE OF INVENTION: Related Thereto
CORRESPONDENCE 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 760; DB 7; Length 156; Best Local Similarity 100.0%; Pred. No. 1.5e-75; Matches 148; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-08-497-214A-2
Sequence 2, Application US/08497214A
Sequence 2, Application US/08497214A
Sequence 2, Application US/08497214A
Sequence 2, Application
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Hannon, Gregory
TITLE OF INVENTION: Cell-cycle Regulatory Proteins and
TITLE OF INVENTION: Cell-cycle Regulatory
UNMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-7401
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley, Hoag & Eliot LLP STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511
FILING DATE: 14-SEP-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-306-511-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boston
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ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,214A
FILING DATE: 30-JUNE-1995
ATTONEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REGISTRATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEPHONE: (617) 832-1000
TELEPHONE: (617) 832-1000
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
TOPPOLOGY: linear
SOB-497-214A-2
```

ö Gaps 1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGA 60 ; 0 Query Match
Best Local Similarity 100.0%; Score 760; DB 8; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.5e-75;
Matches 148; Conservative 0; Mismatches 0; Indels

9 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIOVWMGSARVAELLLHGA 68

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Search completed: May 7, 2002, 12:35:37 Job time: 207 sec

Tue May

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2002, 12:32:40 ; Search time 8.7 Seconds (without alignments) 239.553 Million cell updates/sec Run on:

US-09-016-869B-35

1 MEPSADWLATAAARGRVEEV.....TRGSNHARIDAAEGPSDIPD 148 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

64870 seqs, 14081815 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/USO3_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:* Database ;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1 Sequence 41, App.	2, 4	7	41,	Sequence 1908		12,	4, 4	4	13,	13,	8,	Sequence 8,	Sequence 6,		11,	1 Sequence 11, Appl	14,	Sequence	Sequence 1907		Sequence 6,	Sequence 8,	3 Sequence 23,	268 Sequence 1268	70 Sequence 470, A
SUMMARIES	ΙD	PCT-US02-07826-4	US-09-947-206D-2	US-09-947-206C-2	US-10-097-340-41	US-10-113-872-1908	Ч	US-09-947-206C-13	ı	US-09-947-206C-4	US-09-947-206D-13	US-09-947-206C-1	US-09-947-206D-8	US-09-947-206C-8	US-09-947-206D-6	US-09-947-206C-6	US-09-947-206D-1	US-09-947-206C-1	US-09-947-206D-14	US-09-947-206C-1	US-10-113-872-1907	PCT-US02-09288-13	US-09-972-115A-6	US-09-972-115A-8	PCT-US02-09288-2:	US-09-573-655B-1;	PCT-US02-09944-4
	DB					9															-						-
	Length	156	156	156	156	156	157	157	137	137	138	138	77	77	125	125	82	82	127	127	168	1360	1166	1327	395	844	1536
æ	Query	99.1	99.1	99.1	99.1	99.1	82.6	82.6	64.9	64.9	50.3	50.3	46.8	46.8	43.4	43.4	39.4	39.4	39.4	39.4	30.1	19.7	19.2	18.0	17.9	17.2	17.0
	Score	753	753	753	753	753	627.5	627.5	493.5	493.5	382	382	356	356	330	330	299.5	299.5	299.5	299.5	228.5	149.5	146	137	136	3	129
	Result No.	П	7	m	4	S	9	7	80	60	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56

Sequence 2, Appli Sequence 451, App	Sequence 708, App	4	Sequence 941, App	Sequence 6, Appli	Sequence 26, Appl	Sequence 2, Appli	Sequence 427, App	Sequence 4, Appli	Sequence 696, App	Sequence 778, App	Sequence 514, App	_	Sequence 2, Appli	Sequence 452, App	Sequence 123, App	Sequence 7, Appli	Sequence 40, Appl
US-09-972-115A-2 PCT-US02-09944-451	PCT-US02-09944-708	PCT-US02-09944-429	US-09-573-655B-941	US-10-117-229-6	PCT-US02-09288-26	US-10-117-229-2	PCT-US02-09944-427	US-09-972-115A-4	PCT-US02-09944-696	PCT-US02-09944-778	US-60-365-384-514	US-60-365-384-515	US-60-371-507-2	PCT-US02-09944-452	US-10-002-945-123	US-10-117-229-7	US-10-002-945-40
5	⊣,	Η,	5	9	-	9	Н	S	٦	П	7	7	7	٦	9	9	9
1333	608	182	877	1715	1715	1715	556	1267	1270	2067	305	305	784	1060	654	1762	699
16.6 16.4	16.4	16.1	15.9	14.9	14.8	14.8	14.7	14.7	14.5	14.5	14.4	14.4	14.4	14.4	14.2	14.2	14.1
126 124.5	124.5	122	121	113.5	112.5	112.5	112	111.5	110	110	109.5	109.5	109.5	109.5	108	108	107
27	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	14	45

ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc. et al.

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,

TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer

FILE REFERENCE: MRI-030PC

CURRENT PEDICATION NUMBER: PCT/US02/07826

CURRENT FILING DATE: 2002-03-14

PRIOR PELICATION NUMBER: 60/235,149

PRIOR PLILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: 60/235,149

PRIOR APPLICATION NUMBER: 60/325,149

PRIOR PLILING DATE: 2001-09-27

PRIOR PLILING DATE: 2001-09-27

PRIOR PLILING DATE: 2001-09-19

PRIOR PLILING DATE: 2001-09-26

PRIOR PLILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 41

FENTING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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99.3%; Pred. No. 1.1e-69;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                       Sequence 41, Application PC/TUS0207826 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.34
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
ULT 1
-US02-07826-41
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AFFLACANT:

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,

TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer

FILE REFERENCE: MRI-030

CURRENT APPLICATION NUMBER: US/10/097,340

CURRENT FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-09-26

PRIOR PELICATION NUMBER: 60/276,026

PRIOR PELICATION NUMBER: 60/276,026

PRIOR PELING DATE: 2001-03-14

PRIOR PELING DATE: 2001-03-14

PRIOR FILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-09-16

PRIOR PELING DATE: 2001-09-26

PRIOR PELING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 363

SEQ ID NO 41

SEQ ID NO 41

LEGGTH: 156

LEGGTH: 156

LEGGTH: 156

LEGGTH: 156

LEGGTH: 156

LEGGTH: 156
                                                                                                                                                                                                                                                                                                        1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 156;
                                                                                                                                           Length 156;
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                                                                                                                                           Score 753; DB 5;
Pred. No. 1.1e-69;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                 121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                         129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 41, Application US/10097340; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steve G. KOVATS
Rachel E. MEYERS
MICHAEL MORRISEY
PETER OLANDT
Ami SEN
PETER VEIBY
Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manjula GANNAVARAPU
Sebastian HOERSCH
Shubhangi KAMATKAR
                                                                                                                                             99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosemarie SCHMANDT
Xumei ZHAO
Karen GLATT
                                                                                                                                                  Query Match 99.1
Best Local Similarity 99.3
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: John MONAHAN
                                                              , ORGANISM: Homo sapiens
US-09-947-206C-2
SEQ ID NO 2
LENGTH: 156
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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APPLICANT: Beach, D.

APPLICANT: Demetrick, D.

APPLICANT: Serrano, M.

APPLICANT: Serrano, M.

APPLICANT: Hannon, G.

TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO FILE REFERENCE: COKI-19-10-09-04

FILE REFERENCE: COKI-19-10-09-04

FILE REFERENCE: DATE: 1994-05-25

PRIOR PLICATION NUMBER: 08/248,812

PRIOR PLICATION NUMBER: 08/227,371

PRIOR PLICATION NUMBER: 08/154,915

PRIOR PLICATION NUMBER: 07/991,997

PRIOR PLICATION NUMBER: 07/991,997
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Pred. No. 1.1e-69;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
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                                                                  Sequence 2, Application US/09947206D GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.1 Best Local Similarity 99.3 Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-947-206D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-947-206C-2
                                                       US-09-947-206D-2
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PRIOR FILING DATE: 1994-04-14
PRIOR PELING DATE: 1993-10-08/154,915
PRIOR PELING DATE: 1993-11-08
PRIOR RELING DATE: 1992-12-17
PRIOR APPLICATION NUMBER: 07/961,308
PRIOR APPLICATION NUMBER: 07/963,308
PRIOR PILING DATE: 1992-10-16
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 12
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.68;
83.98;
                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 82.69
Best Local Similarity 83.99
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-947-206C-12
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SEQ ID NO 12
LENGTH: 157
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APPLICANT: Beach, D.
APPLICANT: Benetrick, D.
APPLICANT: Serrano, M.
APPLICANT: Gerrano, M.
APPLICANT: Hannon, G.
TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO FILE REFERENCE: GPCI-P14-07, 206D
CURRENT APPLICATION NUMBER: US/09/947, 206D
PRIOR APPLICATION NUMBER: 08/248, 812
PRIOR APPLICATION UNBER: 08/248, 812
PRIOR APPLICATION NUMBER: 08/227, 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                           ó;
                                                                                                                                                            61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 MEDSADWILATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVWAMGSARVAELLLEHGA 68
                           0; Gaps
                                                                                                 9 MEPSADWILATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVWMGSARVAELLLLHGA 68
                                                                        1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Watanabe, Voshihiro
APPLICANT: Watanabe, Voshihiro
APPLICANT: Alada, Michael D.
APPLICANT: Sleath, Paul R.
APPLICANT: Gleath, Paul R.
APPLICANT: Garter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Targe Gary R.
FILE REFERENCE: 21011.478C19
CURRENT APPLICATION NUMBER: US/10/113,872
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 156,
  99.3%; Pred. No. 1.1e-69;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.1%; Score 753; DB 6; 99.3%; Pred. No. 1.1e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                    129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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  Best Local Similarity 99.3
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-10-113-872-1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-10-113-872-1908
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OTHER INFORMATION: Alternate general formula representing amino acid sequence of CTHER INFORMATION: CCR-protein
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(157)
OTHER INFORMATION: Xaa=unknown amino acid residue
US-09-947-206D-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Beach, D.
APPLICANT: Demetrick, D.
APPLICANT: Serrano, M.
APPLICANT: Hannon, G.
TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
FILE REFERENCE: GCT-P14-071
CURRENT APPLICATION NUMBER: 08/248,812
PRIOR FILING DATE: 1994-05-25
PRIOR FILING DATE: 1994-06-25
PRIOR FILING DATE: 1994-04-14
PRIOR FILING DATE: 1993-11-08
PRIOR FILING DATE: 1993-11-08
PRIOR FILING DATE: 1992-12-17
PRIOR FILING DATE: 1992-10-16
NUMBER: OF SEQ ID NOS: 30
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                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             9 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGXXXVAXLLXXXGA 68
                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                          Length 157;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                       Score 627.5; DB 5;
Pred. No. 5.5e-57;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 RYLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09947206C, GENERAL INFORMATION:
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GENERAL INFORMATION:

APPLICANT: Beach, D.

APPLICANT: Demetrick, D.

APPLICANT: Demetrick, D.

APPLICANT: Beach, M.

APPLICANT: Serrano, M.

APPLICANT: GELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
FILE REPERENCE: SOCI-19-104

FILE REPERENCE: SOCI-19-104

CURRENT FILING DATE: 2001-09-04

PRIOR PLICATION NUMBER: 08/294,812

PRIOR PLICATION NUMBER: 08/227,371

PRIOR FILING DATE: 1994-06-25

PRIOR PLICATION NUMBER: 08/154,915

PRIOR PLICATION NUMBER: 08/154,915

PRIOR PLILING DATE: 1993-11-08

PRIOR PLILING DATE: 1992-11-01

PRIOR PLILING DATE: 1992-10-17

PRIOR FILING DATE: 1992-10-16

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 13

LENGTH: 138

**COLD NO 13

LENGTH: 138
                                        APPLICANT: Serrano, M. APPLICANT: Hannon, G. TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 CADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERGHRDVAGYLR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 CADPATLIRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLR 123
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nes 17;
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Pred. No. 1.8e-
3; Mismatches
                                                                                                              TITLE OF INVENTION: CELL CITCL CORREW APPLICATION NUMBER: US/09/947,206C CURRENT FILING DATE: 2001-09-04 PRIOR APPLICATION NUMBER: U8/248,812 PRIOR FILING DATE: 1994-05-25 PRIOR FILING DATE: 1994-06-25 PRIOR FILING DATE: 1994-04-14-14 PRIOR APPLICATION NUMBER: 08/227,371 PRIOR FILING DATE: 1993-11-08 PRIOR FILING DATE: 1993-11-08 PRIOR FILING DATE: 1992-11-17 PRIOR FILING DATE: 1992-10-16 PRIOR FILING DATE: 1992-10-16 SPIOR FILING DATE: 1992-10-16 PRIOR FILING PARE: PARENT NOS: 30 PRIOR FILING PARENT NOS: 30 PRIOR PRIOR PARENT NOS: 30 PRIOR PARENT PAR
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.9%;
83.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 83.1
Matches 103; Conservative
                          Demetrick, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-947-206C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
APPLICANT: Beach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 TATG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L24 AAAG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                           9 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMMGXXXVAXLLXXGA 68
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                                                                                                              Length 157;
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                                                                                                                                                                       23; Indels
                                                                                                              Score 627.5; DB 5;
Pred. No. 5.5e-57;
0; Mismatches 23;
; OTHER INFORMATION: Xaa-unknown amino acid residue US-09-947-206C-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 RYLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 XYLRXAXGGTRGSNHARIDAAEGPSDIPD 157
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US-09-947-206C-4
'S-quence 4, Application US/09947206C
', GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09947206D
GENERAL INFORMATION:
APPLICANT: Beach, D.
APPLICANT: Demetrick, D.
                                                                                                                82.6%;
83.9%;
                                                                                                                                                                          Conservative
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                                                                                                                Query Match
Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 TATG 136
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US-09-947-206D-4
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APPLICANT: Dead.i.
APPLICANT: Dead.i.
APPLICANT: Dead.i.
APPLICANT: Dead.i.
APPLICANT: Serrano, M.
APPLICANT: Hannon, G.
TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
FILE REFERENCE: GPOI-09-04
CURRENT APPLICATION NUMBER: U8/29/947,206C
CURRENT FILING DATE: 1994-06-5-25
PRIOR APPLICATION NUMBER: 08/248,812
PRIOR FILING DATE: 1994-04-14
PRIOR FILING DATE: 1994-04-14
PRIOR FILING DATE: 1993-11-08
PRIOR FILING DATE: 1993-11-08
PRIOR FILING DATE: 1993-11-08
PRIOR APPLICATION NUMBER: 07/991,997
PRIOR FILING DATE: 1993-11-08
PRIOR FILING DATE: 1992-10-16
PRIOR APPLICATION NUMBER: 07/991,997
PRIOR FILING DATE: 1992-10-16
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SCREAMON, M.
APPLICANT: SCREAMON, M.
APPLICANT: SCREAMON, M.
TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
FILE REFERENCE: GPCI-P14-071
CURRENT FILING DATE: 2001-09-04
CURRENT FILING DATE: 1994-05-25
PRIOR FILING DATE: 1994-05-25
PRIOR FILING DATE: 1994-04-14
PRIOR FILING DATE: 1992-10-16
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 30
        73 CXDPXTXXXRPVHDAAREGFLDTLVVLHXXGARLDVRDAWGRLPXDLAXEXGHXDXXXYL 132
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Pred. No. 7.5e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09947206C GENERAL INFORMATION:
APPLICANT: Beach, D.
APPLICANT: Demetrick, D.
                                                                                                                                                                                                                                               Sequence 8, Application US/09947206D GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.8%;
ilarity 93.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 FLDTLVVLHRAGARLDV 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 72; Conserv
                                                            123 RAAAG 127
                                                                                                             133 RXAXG 137
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US-09-947-206D-8
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        В
                                                            δλ
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OTHER INFORMATION: Alternate general formula representing the amino acid sequence of
OTHER INFORMATION: CCR-protein
; OTHER INFORMATION: Alternate general formula representing the amino acid sequence of CTHER INFORMATION: CCR-protein
; NAME/RE: MISC_FEATURE
; LOCATION: (1)..(138)
; OTHER INFORMATION: Xaa=unknown amnio acid residue
US-09-947-206D-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-UY-94/-ZUBC-13

Sequence 13, Application US/09947206C

GENERAL INFORMATION:

APPLICANT: Beach, D.

APPLICANT: Beach, D.

APPLICANT: Beach, D.

APPLICANT: Beach, D.

TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
FILE REFERENCE: GPC-1944-071

CURRENT APPLICATION NUMBER: US/09/947,206C

CURRENT FILING DATE: 1934-05-25

PRIOR PELICATION NUMBER: 08/227,371

PRIOR PELICATION NUMBER: 08/227,371

PRIOR PELICATION NUMBER: 08/227,371

PRIOR PELICATION NUMBER: 09/154,915

PRIOR PELING DATE: 1993-11-08

PRIOR PELING DATE: 1993-11-07

PRIOR PELING DATE: 1992-10-16

SOFTWARE PELICATION NUMBER: 07/991,997

PRIOR FILING DATE: 1992-10-16

NUMBER: 07/963,308

PRIOR PELING DATE: 1992-10-16

SOFTWARE: PALECATION NUMBER: 07/963,308

SOFTWARE: PALECATION NUMBER: 07/963,308
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Pred. No. 3.5e-32;
3; Mismatches 36; Indels
                                                                                                                                                                                                                        Score 382; DB 5; Length 13
Pred. No. 3.5e-32;
3; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COTHER INFORMATION: Xaa=unknown amnio acid residue US-09-947-206C-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.3%;
Best Local Similarity 67.2%;
Matches 84; Conservative
                                                                                                                                                                                                                        Query Match 50.3%;
Best Local Similarity 67.2%;
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 RAAAG 127
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US-09-947-206C-13
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Search completed: May 7, 2002, 12:35:52 Job time: 192 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus US-09-947-206c-6
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Sequence 6, Application US/09947206D

GENERAL INFORMATION:
APPLICANT: Beach, D.
APPLICANT: Beach, D.
APPLICANT: Beach, D.
APPLICANT: Beach, D.
APPLICANT: Handon, G.
TITLE OF INVENTION: CELL-CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
FILE REFERENCE: GPCI-P14-071
CURRENT PAPLICATION NUMBER: US/09/947,206D

FILMS APPLICATION NUMBER: 08/248,812,
PRIOR FILING DATE: 1994-04-14
PRIOR PRIOR PELING DATE: 1994-04-14
PRIOR FILING DATE: 1994-04-14
PRIOR FILING DATE: 1993-11-08
PRIOR FILING DATE: 1993-10-16
PRIOR FILING DATE: 1992-10-16
SOFTWARE: PALENTING NUMBER: 07/963,308
PRIOR FILING DATE: 1992-10-16
SOFTWARE: PALENTIN VUMBER: 07/963,308
                                                                                                                                                                                                                                                            ó;
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                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                            22 ALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREG 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.4%; Score 330; DB 5; Length 125; 60.7%; Pred. No. 5.8e-27; Live 12; Mismatches 24; Indels
                                                                                                                                                                                                             Length 77;
                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                      Score 356; DB 5;
Pred. No. 7.5e-30;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 6, Application US/09947206C; GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                      Query Match
Best Local Similarity 93.5%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       82 FLDTLVVLHRAGARLDV 98
                                                                                                                                                                                                                                                                                                                                                                                                               61 FLDTLVVLHRAGARLDV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68; Conservative
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APPLICANT: Demetrick, D.
APPLICANT: Serrano, M.
                                                                                         ; TYPE: PRT; ORGANISM: Mus musculus US-09-947-206C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus US-09-947-206D-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 68; Conserve
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US-09-947-206C-6
                                            SEQ ID NO 8
LENGIH: 77
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| TITLE OF INVENTION: CELL.CYCLE REGULATORY PROTEINS, AND USES RELATED THERETO
| FILE REPRENUE: GFOCT-F14-071
| FILE PREPRENUE: GFOCT-F14-071
| CURRENT PAPILICATION NUMBER: US/09/947,206C
| CURRENT FILING DATE: 199-04-04-04-04-04
| PRIOR APPLICATION NUMBER: 08/22/371
| PRIOR APPLICATION NUMBER: 07/921,371
| PRIOR PELLING DATE: 1993-11-08
| PRIOR PELLING DATE: 1993-11-08
| PRIOR PELLING DATE: 1993-11-08
| PRIOR PELLING DATE: 1992-12-17
| PRIOR PELLING DATE: 1992-12-16
| PRIOR PELLING DATE: 1992-10-16
| PRIOR PELLING DATE: 1993-11-08
| PRIOR PELLING DELIVERAGES CENCRAGNECTAGNUAD DELIVERD PERDORPHICE DATE: PRIOR PELLING DELIVERD PELLING PERDORPHICE DELIVERD PER
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us-09-016-869b-35.rai

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May 7, 2002, 12:30:35; Search time 12.51 Seconds (without alignments) 266.226 Million cell updates/sec
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Sequence 16, Appl
Sequence 24, Appl
Sequence 4, Appli
Sequence 2, Appli
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Appli
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                                                                                                                                                                                                                                                                      760
1 MEPSADWLATAAARGRVEEV......TRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, A Sequence 3, A Sequence 2, A Sequence 3, A Se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/PcTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-314-106A-16

US-08-314-106A-24

PCT-US93-09945-4

US-08-617-610-2

US-08-637-610-2

US-08-316-11A-2

US-08-316-11A-2

US-08-316-11A-2

US-08-316-11A-2

US-08-316-11A-2

US-08-316-11A-2

US-08-316-11A-2

US-08-316-11A-2

US-08-316-11A-2

US-08-508-08-2

US-08-11A-177-2

US-09-11A-178-2

US-09-11A-178-2

US-09-11A-178-2

US-09-11A-178-2

US-09-11A-178-2

US-09-11A-178-2

US-09-11A-178-2

US-09-11A-178-2

US-09-11A-178-2

US-08-966-51E-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                       212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_AA:*
                                                                                                                                                                                                                                           US-09-016-869B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                   Sednence:
                                                                                                                                                 Run on:
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Sequence 12, Appl	Sequence 14, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli												
US-08-581-918A-12	US-08-474-177-14	US-08-487-033-14	US-08-480-810-14	US-08-508-735-14	US-08-848-251-14	US-08-486-047-14	US-09-120-130-14	US-09-115-252-14	US-08-986-515-14	US-09-120-128-14	US-09-120-129-14	US-09-201-139-14	US-09-120-131-14	US-08-627-610-8	US-08-581-918A-8	US-08-346-147B-8
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157	105	105	105	105	105	105	105	105	105	105	105	105	105	130	130	130
82.6	71.6	71.6	71.6	71.6	71.6	71.6	71.6	71.6	71.6	71.6	71.6	71.6	71.6	70.1	70.1	70.1
627.5	544	544	544	544	544	544	544	544	544	544	544	544	544	533	533	533
28	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 4, Application US/08154915

Patent No. 5618669

GENERAL INFORMATION:
APPLICANT: Beach, David
APPLICANT: Xiong, Yue
TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION 1873

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-CAT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1993

PRIOR APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1993
ATTORNEY AGENT INFORMATION:
AMADE: VIECLE APPLICATION NUMBER: US 07/701,514
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,915
FILING DATE: 19-NOV-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPRAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 148 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                            usa
                                                                                                                                                                                                                                                                                                                                                               02109
                                                                                                                                                                                                                                                                                                               STATE: MA
COUNTRY: U
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Sequence Sequence

US-08-910-722-2 PCT-US96-05252-

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APPLICANT: Sherr Ph.D., Charles J.
APPLICANT: Downing M.D., James
APPLICANT: Downing M.D., James
APPLICANT: Hirsh Ph.D., Hiroshi
APPLICANT: Okuda, Tsukasa
TITLE OF INVENTION: Infac-pl8 and Infad-P19, Inhibitors of
TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
WUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLABELGHRDVAR 120
    EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                        61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1:30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,106A
FILING DATE: 06-FEB-1994
CLASSIFTANTON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 760; DB 3;
100.0%; Pred. No. 1.5e-83;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           IE: STERNE, KESSLER, GOLDSTEIN & FOX 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0656.0500000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                           121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                       RESULT 3
US-08-384-106A-24
Sequence 24, Application US/08384106A
Patent No. 6033847
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-260
TELEPAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 148 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.1
Best Local Similarity 100.1
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: lir; MOLECULE TYPE: US-08-384-106A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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Sequence 16, Application US/08384106A

Patent No. 6033847

GENERAL INFORMATION:

APPLICANT: Sherr Ph.D., Charles J.

APPLICANT: Browning M.D., James

APPLICANT: Hiral Ph.D., Hiroshi

TITLE OF INVENTION: InK4C-p18 and InK4d-P19, Inhibitors of

TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and Uses Thereof

TITLE OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX

STREET: 1100 New York Ave., N.W.

CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEDSADWILATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMGSARVAELLLHGA 60
                                                                                                                                                    1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
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                                                                        Length 148;
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                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,106A
FILING DATE: 06 FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                        100.0%; Score 760; DB 1; 100.0%; Pred. No. 1.5e-83;
                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
TATORNEY/AGENT INFORMATION:
NAME: FOX, Samuel L
REGISTRATION NUMBER: 30,353
REFERENCE/POCKET NUMBER: 0656.0500000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                 121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 148 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202-371-2540
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-384-106A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005
COMPUTER READABLE FORM:
    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                              Best Local Similarity
Matches 148; Conserv
; MOLECULE TYPE:
US-08-154-915-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                            Query Match
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61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              Length 156;
                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 760; DB 2; 100.0%; Pred. No. 1.6e-83;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                               NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERNCE/DOCKET NUMBER: CSI-001CP6
TELECOMMUNICATION: TELECOMMUNICATION: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08306511A
Patent No. 5962316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: LAHIVE & COCKFIELD 60 State Street
                                                                                                                              TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
          CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 148; Conservative
                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-627-610-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                           TITLE OF INVENTION: Cyclin Complex Rearrangement and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-627-510-2

US-08-627-510-2

Sequence 2, Application US/08627610

Patent No. 5919997

GENERAL INFORMATION:

APPLICANT: Beach, David H.

APPLICANT: Serrano, Manuel I.

APPLICANT: Depinho, Ronald A.

TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle

TITLE OF SEQUENCES:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 760; DB 5;
100.0%; Pred. No. 1.5e-83;
tive 0; Mismatches 0;
                                                                                                                                                                                                                  SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
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                   Sequence 4, Application PC/TUS9309945 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 148 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein PCT-US93-09945-4
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PCT-US93-09945-4
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TELEFAX: (617) 832-7000 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 156 amino acids
                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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STATE: MA
COUNTRY: US
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US-08-581-918A-2
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                                                                                                                                                                                                                                                                                                                                                                       69 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                 1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                              ..
                                                                                                                       Length 156;
                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Beach, David H.
APPLICANT: Benetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Grano, Manuel
APPLICANT: Grano, Manuel
APPLICANT: Grano, Manuel
APPLICANT: Grano, Manuel
TITLE OF INVENTION: Gell-Cycle Regulatory Proteins,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                  100.0%; Score 760; DB 2;
100.0%; Pred. No. 1.6e-83;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/893,274

FILING DATE: 15-JULY-1997

CLASSIFICATION BOD ATA:

APPLICATION NUMBER: US 08/306,511

FILING DATE: 14-SEPTEMBER-1994

FILING DATE: 14-SEPTEMBER-1994

FILING DATE: 25-MAX-1994

PRIOR APPLICATION NUMBER: US 08/248,812

FILING DATE: 15-MAX-1994

PRIOR APPLICATION NUMBER: US 08/24,915

FILING DATE: 14-APPLI-1994

PRIOR APPLICATION NUMBER: US 08/27,371

FILING DATE: 14-APPLI-1994

PRIOR APPLICATION NUMBER: US 08/27,371

FILING DATE: 14-APPLI-1994

PRIOR APPLICATION NUMBER: US 08/21,371

FILING DATE: 11-APPLI-1994

PRIOR APPLICATION NUMBER: US 08/21,4915

PRIOR APPLICATION NUMBER: US 08/154,915

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/154,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08893274 Patent No. 5968821 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,7
                                                                                                                                              Best Local Similarity 100.
Matches 148; Conservative
        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                 ;
US-08-306-511A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-893-274-2
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                                                                                                                       Query Match
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Gaps
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APPLICANT: Beach, David H.
APPLICANT: Benetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                           Length 156;
                                                                                                                                        Indels
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O
                                                                                           100.0%; Score 760; DB 2;
100.0%; Pred. No. 1.6e-83;
iive 0; Mismatches 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: U2-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION UMBER: US 08/346,147
FILING DATE: 14-SEP-1994
FILING DATE: 14-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                            129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
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FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 148; Conservative
, MOLECULE TYPE: protein US-08-893-274-2
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us-09-016-869b-35.rai

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GENERAL INFORMATION:
APPLICANT: Massague, Joan
APPLICANT: Roberts, James M.
APPLICANT: Roberts, James M.
APPLICANT: Roff, Andrew
APPLICANT: Roff, Andrew
APPLICANT: Polyak, Kornelia
TITLE OF INVENTION: Isolated P27 Protein, Nucleic Acid
TITLE OF INVENTION: Molecules Encoding Same, Methods of Identifying Agents Acti
TITLE OF INVENTION: and Uses of Said Agents
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,936
FILING DATE: 21-FEBRUARY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/POCKET NUMBER: 36,709
REFERENCE/POCKET NUMBER: 36,709
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION (1872-1000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , DB 4;
1.6e-83;
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Pred. No. 1
                                      FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
PAPLICATION DATA:
PELLING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: VINCent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 31,709
REFERENCE/DOCKET NUMBER: 31,709
REFERENCE/OCKET NUMBER: 31,709
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 832-1299
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STREET: One Post Office Square
CITY: Boston
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100.0%;
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Best Local Similarity 100.
Matches 148; Conservative
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ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Beach, Douglas J.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,147B
FILING DATE: 29-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
                                                                                            NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,7709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 832-1299
TELEFAN: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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FILING DATE: 25-MAY-1994
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                         US 07/991,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08346147B Patent No. 6211334
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                                           FILING DATE: 17-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              ENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-581-918A-2
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 148; Conservative
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PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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STATE: MA
COUNTRY: US
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US-08-346-147B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMMGSARVAELLLHGA
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US 08/154,915
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EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
                                               61 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 120
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                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08589981
Patent No. 5672508
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Lamphere, Lou
APPLICANT: Lamphere, Lou
TITLE OF INVENTION: Inhibitors of Cell-Cycle Progression,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPES: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,981
                                                                                                                                                                    129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                    121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148
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REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-OFFECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-08474-177-2
Sequence 2, Application US/08474177
; Patent No. 5624819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-589-981-2
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STATE: MA
COUNTRY:
                                                                                                                                                                                                                                                                                      RESULT 12
US-08-589-981-2
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                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLHGA 60
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                                                                                                                                                                                                                                                                                                               Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
100.0%; Score 760; DB 5; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 760; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.6e-83;
Matches 148; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION DATA: 14-58P-1994
PRIOR APPLICATION DATA: APPLICATION DATA: 15-NAY-1994
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: 1994
PRIOR APPLICATION DATA: A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS9504636
GENERAL INFORMATION;
APPLICANT:
TELEFAX: (617) 832-7000 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
                                                                                        LENGTH: 156 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECCLE TYPE: protein
US-08-822-936-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
PCT-US95-04636-2
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Sequence 2, Application US/08487033 Patent No. 5739027
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REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                    ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                        CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Matches 147; Conserv
                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-487-033-2
RESULT 14
US-08-487-033-2
                                                                                                                                                                                                                                                                   COUNTRY:
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          APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb. Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPENDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 Naw York Avenue, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/474,177 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 753; DB 1;
Pred. No. 1.1e-82;
0; Mismatches 1;
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FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 99.3%;
Matches 147; Conservative (
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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GY: linear
  GENERAL INFORMATION:
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STATE: D
COUNTRY:
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9 MEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVWMMGSARVAELLLEHGA 1 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 99.1%; Score 753; DB 1; Length 156; ilarity 99.3%; Pred. No. 1.1e-82; Conservative 0; Mismatches 1; Indels 3: Venable, Baetjer, Howard & Civiletti, LLP 1201 New York Avenue, Suite 1000 MEDIUM TIPE: FIDEPY GISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Patentin Release #1.0, Version #1.30
CUSRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-VUN-1995
CLASSITCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/217,369
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
ANAWER: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
ANAWER: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
ANAWER: 18-MAR-1994
ATTORNEY/AGENT INFORMATION: 24884-109348-C 121 YLRAAAGGTRGSNHARIDAAEGPSDIPD 148 129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156 GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
ITILE OF INVENTION: MTS1E1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:

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             Sequence 2, Application US/08480810
| Patent No. 5801236
| GENERAL INFORMATION:
| APPLICANT: Ramb, Alexander
| TITLE OF INVENTION: MTS1 GENE
| NUMBER OF SEQUENCES: 36
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: Mashington
| STREET: 1201 New York Avenue, Suite 1000
| STATE: DC | COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
99.1%; Score 753; DB 1; Length 156;
Best Local Similarity 99.3%; Pred. No. 1.1e-82;
Matches 147; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/480,810
FILING DATE: US/-JUN-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17 MAR-1995
PRIOR APPLICATION NUMBER: DCT/US95/03316
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION USATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY ABAR-1994
ATTORNEY ABAR-1994
ATTORNEY AGENT INFORMATION:
AMAN: Those Tables Those Tables Those
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REGISTRATION UNBER: 28,957
REFERENCE/DOCKET UNBER: 2488
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-962-4810
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-480-810-2
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US-08-480-810-2
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DD 129 YLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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Search completed: May 7, 2002, 12:33:23 Job time: 168 sec